

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 05:44:31 ; Search time 6820 Seconds
(without alignments)
11377.025 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcggagagag.....tatggcatgctcgagctgcg 1365

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1365	100.0	1365	6 AR606281	AR606281 Sequence
2	1365	100.0	1365	6 AX490719	AX490719 Sequence
3	585.8	42.9	1380	15 AX325817	AX325817 Lycopersi
4	584.2	42.8	1747	15 OSU49113	U49113 Oryza sativ
5	583.2	42.7	1417	15 AB039916	AB039916 Vicia fab
6	582.8	42.7	1563	15 AK072676	AK072676 Oryza sat
7	581.8	42.6	1376	15 AK071838	AK071838 Oryza sat
8	581	42.6	1497	15 FSV298829	AJ298829 Fagus syl
9	575.4	42.2	1475	15 AB039917	AB039917 Vicia fab
10	575	42.1	1370	15 AF107464	AF107464 Hevea bra
11	574.2	42.1	1264	15 ATHPRPHB	M96733 Arabidopsis
12	574.2	42.1	1343	15 AY059847	AY059847 Arabidops
13	573.8	42.0	1092	15 AY093267	AY093267 Arabidops
14	573.6	42.0	1511	15 AV325818	AV325818 Lycopersi
15	561	41.1	1261	15 AY087557	AY087557 Arabidops
16	559.4	41.0	921	6 AX506010	AX506010 Sequence
17	559.4	41.0	952	15 AY096543	AY096543 Arabidops
18	559.4	41.0	1256	15 ATHPRPHA	M96732 Arabidopsis

19	559.4	41.0	1288	15 AY063942	AY06
20	542.4	39.7	1211	15 HAPRPH2A	236C
21	533.4	39.1	1238	15 ATU39568	U395
22	531.8	39.0	924	6 AX505876	AX505
23	518.6	38.0	1708	15 NTNP24	2937
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25	516.8	37.9	1348	5 CR761518	CR761
26	516.8	37.9	2026	5 BC064168	BC064
27	516	37.8	1854	5 AJ719537	AJ719
28	515.6	37.8	2574	6 AR373433	AR373
29	515.6	37.8	2574	8 HUMPP2AB	M6046
30	515.4	37.8	1590	8 BC012022	BC012
31	515	37.7	1869	9 BC058582	BC058
32	514	37.7	1522	6 CQ715253	CQ715
33	513.8	37.6	1589	15 NTA7496	AJ0C
34	513.8	37.6	1723	8 AK091875	AK091
35	513.8	37.6	208762	14 AC160324	AC16
36	513	37.6	1712	5 BC045892	BC045
37	512.4	37.5	1529	6 AX409451	AX409
38	512.4	37.5	1529	8 HUMALPHLB	JO38C
39	512.4	37.5	1541	6 CS129134	CS129
40	512.4	37.5	1541	8 HSP22A	X1265
41	512	37.5	208762	14 AC160324	AC16
42	512	37.5	250768	14 AC163377	AC16
43	510.8	37.4	930	6 AX305485	AX305
44	510.8	37.4	930	8 CR541747	CR541
45	510.8	37.4	930	9 MPMPO2AIB	Z6774

ALIGNMENTS

RESULT 1	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
LOCUS	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
DEFINITION	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
ACCESSION	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
VERSION	AR606281.1	GI:56658183	1365 bp	DNA	linear	EC-2004
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1365)					
AUTHORS	da Costa e Silva.O., Bohnert,H.J., van Thielens,N., C					
TITLE	Phosphatase stress-related proteins and methods of u					
JOURNAL	Patent: US 6818805-A 8 16-NOV-2004;					
	BASF Plant Science GmbH; Ludwigshafen;					
	DEX;					
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Db	1 GCGGTAAACGCGGAGGAGAGCGGATCGTTAGGGTTTGGTGCAGGGC					GA 60
QY	61 GGTGGGCAATCGCGTATATGCAGATGTAGACCGGAGATAGAGCAGC					TG 120
Db	61 GGTGGGCAATCGCGTATATGCAGATGTAGACCGGAGATAGAGCAGC					TG 120
QY	121 CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGA					GT 180
Db	121 CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGA					GT 180
QY	181 GGAGAGTGAACGTCGACGCCCGTGAAGTCTCTGTCAAGTTTCGGTGC					GG 240

Db 181 GGAGAGTGGACGTGACCGCGTGAAGTCTCTGTACGGTTTCGGGTGACATCCATGG 240

Qy 241 CCAGTTTCATGATCTCATCGAGCTTTTCGCAATAGGAGCAAGCGCCGACACGAACTA 300

Db 241 CCAGTTTCATGATCTCATCGAGCTTTTCGCAATAGGAGCAAGCGCCGACACGAACTA 300

Qy 301 CTTGTTTCATGGCGACTATGAGTCTGGATGATTAATTTCTGTCGAGACTGTGTCGCTCTT 360

Db 301 CTTGTTTCATGGCGACTATGAGTCTGGATGATTAATTTCTGTCGAGACTGTGTCGCTCTT 360

Qy 361 AGTGCCCTGAAGGTGCGGTATAGGATAGGATCACAATCTTTCGAGGAAACACGAGAG 420

Db 361 AGTGCCCTGAAGGTGCGGTATAGGATAGGATCACAATCTTTCGAGGAAACACGAGAG 420

Qy 421 CAGGCAGATTACGCAAGTATATGTTTCTATGATGAATGCCCTGCGGAAGTATGGAATGC 480

Db 421 CAGGCAGATTACGCAAGTATATGTTTCTATGATGAATGCCCTGCGGAAGTATGGAATGC 480

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Db 481 GAAATGTTTGGAACTACTTCACGGATCTGTTCCGACTACCTGCCCTCGACAGCTCTCATTTGA 540

Qy 541 GCA CGAGATTTTTTCTGTTTCATGTTGGTCTGTCTCCATCGCTCGACACATTAGATCAAT 600

Db 541 GCA CGAGATTTTTTCTGTTTCATGTTGGTCTGTCTCCATCGCTCGACACATTAGATCAAT 600

Qy 601 CCGAGCCCTAGATCGTATTCAAGAAAGTGC CGACGAGGCGCCGATGTGTGATCTACTCTG 660

Db 601 CCGAGCCCTAGATCGTATTCAAGAAAGTGC CGACGAGGCGCCGATGTGTGATCTACTCTG 660

Qy 661 GTCTCATCCAGATGATCGTTGGATGGGCATTTTCACCAAGAGTGGCGGTATACATTT 720

Db 661 GTCTCATCCAGATGATCGTTGGATGGGCATTTTCACCAAGAGTGGCGGTATACATTT 720

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Db 721 TGGTCAAGATATTGACAGACAGTTCATCATACCAATGTTCTAAATGTTGGTTGCACGTGC 780

Qy 781 TCACAGCTTGTGATGGAAGGATACAAATGTTGGTCCAGGATAAAAAATGTTGTACAGTTTT 840

Db 781 TCACAGCTTGTGATGGAAGGATACAAATGTTGGTCCAGGATAAAAAATGTTGTACAGTTTT 840

Qy 841 CAGTGCCCCCAATTAAGTCTGTTACCGCTGTGGGAACATGGCCGCCATAATGAGATAGTA 900

Db 841 CAGTGCCCCCAATTAAGTCTGTTACCGCTGTGGGAACATGGCCGCCATAATGAGATAGTA 900

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Db 901 AACAAATGAATCGTCTTTTCTTTTTCAGTTTCGAAACAGCACCGCGGCAAAAGTGAACAGATGT 960

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Db 961 GACGGGAAGACTCTCTGATTAATTTCTGTAATCATGGGCTATACATGTAATCTTTTACTT 1020

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Db 1021 ACTGAAATGTTCTGTATAGTACCTTCATGGAACGATTTTCCCTGAAAGAGATACT 1080

Qy 1081 CCCTCATGATCTAGTATGAAGTATCTTCTTTGAAAGTGTTCCTTTTCTTTTAGTA 1140

Db 1081 CCCTCATGATCTAGTATGAAGTATCTTCTTTGAAAGTGTTCCTTTTCTTTTAGTA 1140

Qy 1141 CTTGTCCTCTCTTTCATTCATTAAGTTGCTTCAGAACTGAGATGTTGTGAATGTA 1200

Db 1141 CTTGTCCTCTCTTTCATTCATTAAGTTGCTTCAGAACTGAGATGTTGTGAATGTA 1200

Qy 1201 CTGCGACAAGAGGACGTCTCAATGTTGTCGAGGTTTATAGTATAGGGAAGAGGT 1260

Db 1201 CTGCGACAAGAGGACGTCTCAATGTTGTCGAGGTTTATAGTATAGGGAAGAGGT 1260

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Db 1261 AGCACATGTTACTTCAAATCGATCAGAGACTTCTATGGAAAAAGATGACGATGGTGAAC 1320

Qy 1321 AACGTTTCATCTCCACACTACTGTATATGGCATGCTCGAGCTCGC 1365

Db 1321 AACGTTTCATCTCCACACTACTGTATATGGCATGCTCGAGTCCG 1365

RESULT 2

LOCUS AX490719 1365 bp DNA linear

DEFINITION Sequence 8 from Patent WO0246442.

ACCESSION AX490719

VERSION AX490719.1 GI:22323691

KEYWORDS

SOURCE Physcomitrella patens

ORGANISM Physcomitrella patens

REFERENCE 1

AUTHORS da Costa,E.S., Bohnert,H.J., Ishitani,M., van Thiele: Chan,R.

TITLE Phosphatase stress-related proteins and methods of u.

JOURNAL Patent: WO 0246442-A 8 13-JUN-2002;

BASEL Plant Science GmbH (DE)

FEATURES

Location/Qualifiers

1..1365

/organism="physcomitrella patens"

/mol_type="unassigned DNA"

/db_xref="taxon:3218"

ORIGIN

Query Match 100.0%; Score 1365; DB 6; Length 13;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1365; Conservative 0; Mismatches 0; Indels

Qy 1 GCGCTTAACGCGCGAGAGAGCGGATCGGTTAGGTTTGGTGCAGGGG 3A 60

Db 1 GCGCTTAACGCGCGAGAGAGCGGATCGGTTAGGTTTGGTGCAGGGG 3A 60

Qy 61 GGTGGGCAATCGCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 1G 120

Db 61 GGTGGGCAATCGCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 1G 120

Qy 121 CAACCGTTGTCGAGTTGGAGGTGAAGAACTATGTATCAAGCTCCGA 3T 180

Db 121 CAACCGTTGTCGAGTTGGAGGTGAAGAACTATGTATCAAGCTCCGA 3T 180

Qy 181 GGAGAGTGGAACTGACGCCGTGAAGTGTCTGTACGGTTTTCGGGTG 3G 240

Db 181 GGAGAGTGGAACTGACGCCGTGAAGTGTCTGTACGGTTTTCGGGTG 3G 240

Qy 241 CCAGTTTCATGATCTCATCGAGCTTTTCGGCATAGGAGCAAGGCGCCG 3A 300

Db 241 CCAGTTTCATGATCTCATCGAGCTTTTCGGCATAGGAGCAAGGCGCCG 3A 300

Qy 301 CTTGTTTCATGGCGCACTATGTCGATCGTGGATATTTCTGTCGAGACTG 3T 360

Db 301 CTTGTTTCATGGCGCACTATGTCGATCGTGGATATTTCTGTCGAGACTG 3T 360

Qy 361 AGTGCCCTGAAGGTGCGGTATAGGATAGGATCACAATCTTTCGAGGGA 3G 420

Db 361 AGTGCCCTGAAGGTGCGGTATAGGATAGGATCACAATCTTTCGAGGGA 3G 420

Qy 421 CAGGCAGATTACGCAAGTATATGTTTCTATGATGAATGCCCTGCGGAAGT 3C 480

Db 421 CAGGCAGATTACGCAAGTATATGTTTCTATGATGAATGCCCTGCGGAAGT 3C 480

Qy 481 GAAATGTTTGGAACTACTTCACGGATCTGTTCCGACTACCTGCCCTCGAC 3A 540

Db 481 GAAATGTTTGGAACTACTTCACGGATCTGTTCCGACTACCTGCCCTCGAC 3A 540

Qy 541 GCACGAGATTTTTTCTTCTTCAATGTTGGTGTCTGTCTCCATCGCTCGACAT 3T 600

Db 541 GCACGAGATTTTTTCTTCTTCAATGTTGGTGTCTGTCTCCATCGCTCGACAT 3T 600

QY	601	CCGAGCCCTAGATCGTATTCAAGAAAGTGC	CGGCACGAGGCCCGGATGTGTGATCTACTCTG	660	
Db	800	CCGAGCACTGGACCGGTATACAAGAGGTGC	CACATGAAGGCCCGGATGTGTGATCTCCTATG	859	
QY	661	GTCTGATCCAGATGATCGTTGTGGATGGGCA	TTTTCACACAGAGGTGC	CGGGTTTACTTT	720
Db	860	GTCTGATCCAGACGATCGCTGTGGTGGGAA	TATCACCCTCGGGGGCTGGTTTACACATT	919	
QY	721	TGGTCAAGATATTGGCAGACGAGTTCAATCA	TACATCAATGGTCTAAAGTTTGGTTGCACGTGC	780	
Db	920	TGGACAGGATATAGCATCTCAGTTTAAATCA	CACTAATGGTCTCTCCTGATTTCTAGAGC	979	
QY	781	TCACAGCTTGTGATGGAAGGATACAATTTGG	TGCGCAGGATAAAAAATGTTGTTCACAGTTTT	840	
Db	980	CCATCAGCTTGTTCATGGAAGGTTTAAATTT	GGTGTGTGAGGATAAGAAATGTTGTAACGATT	1039	
QY	841	CAGTGGCCCCAAATTACTGTTTACCGCTGTG	GGGAACATGCGCCGCATATGAGATAGATGA	900	
Db	1040	TAGTGTCTCAAACTATTGTTATCGCTGTGT	ATAATGCGTGCATCCTAGAAATAAGTGA	1099	
QY	901	AAACAATGAATCGGTCTTTTCTTCAGTTT	TCGAACAGCACCGCGGCAAGTGAACACGATGT	960	
Db	1100	AAACATGGAGCAGAAATTTCTTCAGTTTGA	TCCAGCCAGCTCCACGACAGATTGAGCCTGATC	1159	
QY	961	GAGCGGAAGACTCTCGATTACTTTCTGTAAC	993		
Db	1160	TACAAGGAAGACTCCAGACTACTTCTTGT	TAATC 1192		
RESULT 4					
OSU49113	1747 bp mRNA linear PLN 23-MAR-1999				
LOCUS	Oryza sativa protein phosphatase 2A mRNA, complete cds.				
DEFINITION	Oryza sativa protein phosphatase 2A mRNA, complete cds.				
ACCESSION	U49113				
VERSION	U49113.1 GI:1218053				
KEYWORDS	Oryza sativa (indica cultivar-group)				
SOURCE	Oryza sativa (indica cultivar-group)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1. (bases 1 to 1747) Chang, M., Wang, B., Chen, X. and Wu, R. Molecular characterization of catalytic-subunit cDNA sequences encoding protein phosphatases 1 and 2A and study of their roles in the gibberellin-dependent Osamy-c expression in rice Plant Mol. Biol. 39 (1), 105-115 (1999)				
AUTHORS	Chang, M., Wang, B., Chen, X. and Wu, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-FEB-1996) Men-Chi Chang, Plant Biology, Room 317 Biotech. Building, Cornell University, Ithaca, NY 14850, USA				
PUBMED	10080713				
REFERENCE	2. (bases 1 to 1747) Chang, M.-C., Chen, X. and Wang, B. Submitted (13-FEB-1996) Men-Chi Chang, Plant Biology, Room 317 Biotech. Building, Cornell University, Ithaca, NY 14850, USA				
AUTHORS	Chang, M.-C., Chen, X. and Wang, B.				
TITLE	Direct Submission				
JOURNAL	Submitted (13-FEB-1996) Men-Chi Chang, Plant Biology, Room 317 Biotech. Building, Cornell University, Ithaca, NY 14850, USA				
FEATURES	Location/Qualifiers				
source	1. .1747 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="IR36" /db_xref="taxon:39946" /tissue_type="seed" 169. .1089 /codon_start=1 /product="protein phosphatase 2A" /protein_id="AAA91806.1" /db_xref="GI:1218054" /translation="WPSHADLDROISQLBECKFLGEAEVRALCEQAKAILMEENVNP VRSPTVCGDIHQGFQDLLEFRIGDSPTNLFMGDYDRGYTSVEVTLVLVAVK FCILGSLSPSLDNIRALDIQVPHGPMCDLLSPDPCDGMGSPRGAYNG ODIAQOFNHTGLTISRHLQVMEGFNWCQDKNVTVFSAPNYCYRCGNMAAILIG ENNDQNLQFDPAQPDIDPTTKRTPDYFL"				
CDS					
ORIGIN					

Query Match	42.8%	Score	584.2	DB	15	Length	1
Best Local Similarity	73.5%	Pred. No.	1.2e-164				
Matches	745	Conservative	0	Mismatches	268	Indels	
QY	12	CGGAGGAGAGCGGATCGGTTTAGGTTTGGT	GCACAGGGGGGAGGCGCAGAG	YA	71		
Db	110	GGGGCGCCCTGTGAGGAGGAGGAGGAGGAG	GGGAGGAGGAGGAGGAGGAGGAGGAGGAG	YA	169		
QY	72	TGCCGTCTATATGCAGATGTAGACCGGCAG	ATAGAGCAGCTGTTCGGAGTGC	YT	131		
Db	170	TGCCGTGCACCGCGATCTGGACCGGCAGAT	CTCGCAGCTGCGGAGTGC	YG	229		
QY	132	CGGAGTGTGAGGTGAAGAACCTATGTGATC	AAAGCTCGGACGATCTTTGGTG	YA	191		
Db	230	GGGAGGCGGAGGTGAGGGCGCTGTGCGAGC	AGGCGAAGCGGATCTCTCATG	YA	289		
QY	192	ACGTGCACCGCTGAAGTGTCTGTACGGT	TTTGGGGTGACATCCATGGC	YG	251		
Db	290	ACGTGCACCGCTGCGGAGCCCGTCA	CCGTCCTGCGGCGACATCCACGGC	YG	349		
QY	252	ATCTCATCGAGTTTTTCCGCATAGGAGCA	AGGCGCCCGACACGAACTAC	YG	311		
Db	350	ACCTCATCGAGCTCTTCCGCATCGSGGG	GAATCCCCCGACACCACTAC	YG	409		
QY	312	CGGACTATGTGATCGTGGATTAATTTCTG	TCGAGACTGTGTGCTCTTTA	YA	371		
Db	410	GTGACTAGTCGACCGTGTACTATT	CAGTGGAGACTGTTACATTA	YA	469		
QY	372	AGGTGCGGTATAGGATAGGATCAATCT	TTCGAGGGAACACAGAGC	YA	431		
Db	470	AAGTCCGTTATAGAGAGAGAAATCA	AAATATTGAGAGGAAATCACAGAGC	YA	529		
QY	432	CGCAAGTATATGGTTTCTATGATGAAT	GCCTGCGGAAGTATGGAATGCG	YA	491		
Db	530	CCCAAGTGTATGGCTTCTATGACGAA	TGCTTACGGAAGTATGGAATGCA	YA	589		
QY	492	AGTACTTACCGATCTGTTCGACTAC	TGCGCTCTGACAGCTCTCATTTAG	YT	551		
Db	590	AGTACTTCCGCGACTTGTGATTAAT	TATTTGCTCTCACAGCTCTTTGTAGAA	YT	649		
QY	552	TTTGTCTTATGCTGTCTGCTCCATCG	CTCGACACATTAAGTACACATC	YG	611		
Db	650	TTTGCTCCATGGCGCTCTCGCGCT	CATTGGATACATTTGGATTAACATT	YG	709		
QY	612	ATCGTATTCAAGAAAGTGC	CGCACGAGGCGCCGATGTGTGATCTACTCTGG	YG	671		
Db	710	ATCGCATACAGGAGGTCCCTCAT	GAAAGGCCCATGTGTGTATCTTTTGTGG	YG	769		
QY	672	ATGATCGTTTGGATGGGGCAATTT	CACACAGAGTGCCGGTTATTA	YA	731		
Db	770	ACGATCGATGTGGGTGGGAAATTT	CTCCAAGAGGGGCGAGGATACAAAT	YA	829		
QY	732	TGCGACAGCAGTCAATCATACCAAT	GTCTAAAGTTTGTGTCACGTGCT	YG	791		
Db	830	TTGCACACAATTAACCATTAAT	TGACCTTACCCCTTATTTCAAGGGCC	YG	889		
QY	792	TGATGGAAGGATACAATTTGGT	GCCAGGATAAAATTTGTTCACAGTTTTC	YA	851		
Db	890	TGATGGAAGGCTTCAATTTGGT	GCCAGGACAAGAACGTTGTCA	YA	949		
QY	852	ATTACTGTTCGCTGTGGAAACAT	TGGCGGCCATTAATGGAGATAGTA	YC	911		
Db	950	ACTACTGTTCGCTGTGGTAACT	AACATGCGCAGCAATTTCTAGAAAT	YC	1009		
QY	912	GCTCTTTTCTTCAGTTCGAAC	CAGCACCGCGCAAGTGAACCATGTG	YA	971		
Db	1010	AGAACTCTTACAGTTTCGAT	CAGCCCCACGACAAATAGACCCGACACA	YA	1069		
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Db	1070	CCCCCGACTATTTTTTGT	TAATCGTGGCGTTGACCTTTTTTTTTTAACTC				


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RESULT 5
AB039916
LOCUS      AB039916                1417 bp      mRNA      linear      PLN 15-MAR-2000
DEFINITION Vicia faba vFP2Ac-1 mRNA for type 2A protein phosphatase-1,
complete cds.
ACCESSION  AB039916
VERSION     vFP2Ac-1; GI:7248358
KEYWORDS    type 2A protein phosphatase-1.
SOURCE      Vicia faba (fava bean)
ORGANISM    Vicia faba
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
            Vicia.
REFERENCE   1 (bases 1 to 1417)
AUTHORS    Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.
TITLE       Type 2A protein phosphatase from guard cells of Vicia faba
JOURNAL     Published Only in DataBase (2000)
REFERENCE   2 (bases 1 to 1417)
AUTHORS    Ueno, H., Kinoshita, T., Asanuma, M. and Shimazaki, K.
TITLE       Direct Submission
JOURNAL     Submitted (08-MAR-2000) Toshinori Kinoshita, Kyushu University,
            Graduate School of Sciences; Ropponmatsu 4-2-1, Fukuoka, Fukuoka
            810-8560, Japan (E-mail: toshinori@box.nc.kyushu-u.ac.jp,
            Tel: 81-92-726-4763 (ex. 4763), Fax: 81-92-726-4644)
FEATURES   Location/Qualifiers
            1..1417
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             /dev_stage="mature"
             /note="synonym: Vicia faba L."
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             /db_xref="GI:7248359"
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polyA_site

ORIGIN
Query Match      42.7%; Score 583.2; DB 15; Length 1417;
Best Local Similarity 76.9%; Pred. No. 2.3e-164;
Matches 711; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 68 ACAATGCCGTCATATGACATGTAGACCGGAGATAGACGCTCGGAGTGCACGCG 127
DB 253 ACGATGCCGCTCTCACGCGGATCTGGATCGGCAGATCGACATCTGATGGAGTGCACGCT 312
QY 128 TTGTCGGAGTTGAGGTGAAGAACCTATGTATCAAGCTCGACGACATCTTGGTGGAGGAG 187
DB 313 CTACCGGAGCGGATGTGAGCGGCTTTCGATCAGGCTAGGCGGATCTTGGTGGAGAG 372
QY 188 TGGAAAGTGCACGCCGTGAAGTGTCTCTGTACCGTTTGGGTGACATCCATGCCAGTTT 247
DB 373 TGGAAAGTTCAACCGGTGAAGTGTCCCGTTACCGTTTGGGTGATATTCAAGGTGAGTTT 432
QY 248 CATGATCTCATGACGCTTTCCGATAGGAGCAAGGCCCGCACGACTACTGTTC 307
DB 433 TATGATCTGATTGAGCTTTTTCGGATAGGAGGAAACGCGCTGACTACTATCTCTTT 492

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QY 308 ATGGCGCATATGTGGATCGTGGATATTATTCTGTGAGACTGTGTGCTGCT 367
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RESULT 6
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LOCUS      AB072676                1563 bp      mRNA      linear
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:JC
            insert sequence.
ACCESSION  AB072676
VERSION     AK072676.1 GI:32982699
KEYWORDS    FLI cDNA; CAP trapper.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
AUTHORS    The Rice Full-Length cDNA Consortium, National Insti
            Agrobiological Sciences Rice Full-Length cDNA Projec
            Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi
            Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooi
            Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K
            Ohtsuki, K., Shihiki, T., Foundation of Advancement c
            Science Genome Sequencing & Analysis Group, Otsomo, Y
            Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda,
            Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie
            Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Ni

```

Ikedo, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
12869764

2 (bases 1 to 1563)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariakawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail:skkuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007]
This clone is one of the 28K full-length cDNA clones from japonica rice.
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oota, N., Ota, Y., Saitoh, H., Sasaki, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

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OY	174 TCTTGGTGGAGGAGTGGAAACCTGCAGCCCGTGAAGTGTCTGTCAACGGT
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LOCUS Fagus sylvatica mRNA for protein phosphatase 2A (pp2A-1 gene).
ACCESSION AJ298829
VERSION AJ298829.1 GI:10638984
KEYWORDS pp2A-1 gene; protein phosphatase 2A.
SOURCE Fagus sylvatica (European beech)
ORGANISM Fagus sylvatica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fagales; Fagaceae; Fagus.
1
Gonzalez,M., Nicolas,C., Lorenzo,O., Nicolas,G. and Rodriguez,D.
Characterization and expression of a protein phosphatase type 2A
regulated by GA3 in dormant Fagus sylvatica seeds
Unpublished
2 (bases 1 to 1497)
Nicolas,C.
Direct Submission
Submitted (02-OCT-2000) Nicolas C., Fisiologia Vegetal, Universidad
de Salamanca, Plaza Doctores de la Reinas/n, 37007 Salamanca, SPAIN
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Best Local Similarity 74.8%; Pred. No. 1.1e-163;
Matches 728; Conservative 0; Mismatches 245; Indels
3 0;
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Db 217 GGTGGGATCTGAGCGTTGAGAGAGAGAGACTGAAAAACGATGCCGTG' 276
QY 90 TAGACCGCAGATAGACGAGCTGTGGAGTGCAGCCGTTGTTCGGAGTTG' 149
Db 277 TGGACCGGTCAGATCGAGCATCTGATGGAGTGCAGCCGTTGCCGGAGCG' 336
QY 150 ACCTATGTGATCAAGCTCGGACCATCTTGGTGGAGGAGTGAACGTCGAG' 209
Db 337 CGCTTTGGGATCAGCGAGAGCGGATCTGGTGGAGGAGTGGACGTAACA' 396
QY 210 GTCTGTCAAGTTTGGGTCAGATCCATGAGCCAGTTTCATGATCTCATC' 269
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LAILEIG

[illegible]

AUTHORS Shin,D.H. and Han,K.-H.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1998) Kumho Life and Environmental Science Laboratory, 572 Seangam-Dong, Kwangsan-Gu, Kwangju 506-712, Korea
FEATURES Location/Qualifiers
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ACCESSION M96733
VERSION M96733.1 GI:166822
KEYWORDS protein phosphatase.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
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1 (bases 1 to 1264)
REFERENCE Arino,J., Perez-Callejon,E., Cunillera,N., Camps,M.,
Ferrer,A.
Protein phosphatases in higher plants: multiplicity
phosphatases in Arabidopsis thaliana
Plant Mol. Biol. 21 (3), 475-485 (1993)
8382968
COMMENT Original source text: Arabidopsis thaliana (library:
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QY 241 CCAGTTTTCATGATCTCATCGAGCTTTTCGCGATAGGAGCAAGCGCGCCGACACCAACTA 300
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LOCUS AY059847
DEFINITION Arabidopsis thaliana similar to protein phosphatase type 2A
(Acig10430; T10024.4) mRNA, complete cds.
ACCESSION AY059847
VERSION AY059847.1 GI:16648954
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE
AUTHORS
Spermatophyta; Magnoliophyta; eudicotyledons; core e
rosids; eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 1343)
Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Iehida,J., Kan
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pha
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (22-OCT-2001) DNA Sequencing and Technoloe
Stanford University, 855 California Avenue, Palo Alt
USA
e-mail for correspondence: arab@sequence.stanford.ec

COMMENT
RIKEN Genomic Sciences Center (GSC) members carried
collection and clustering of RAFL cDNAs (RAFL cDNA :
Arabidopsis Full-length cDNA): Seki,M., Narusaka,M.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members ca
sequencing and annotation of the RAFL cDNAs: Nguyen,
Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chu
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shir
Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) con
equally to this work. Shinozaki,K. (RIKEN GSC) and
(SSP/Stanford) contributed equally to this work as

FEATURES

Location/Qualifiers

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ORIGIN

Query Match 42.1%; Score 574.2; DB 15; Length 1
Best Local Similarity 76.0%; Pred. No. 1.2e-161;
Matches 708; Conservative 0; Mismatches 223; Indels

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QY 241 CCAGTTTTCATGATCTCATCGAGCTTTTCCGATAGGAGCAAGCGCCG 300
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edons;
M.,
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304,

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J.,
w.

EYVNVQV
LIVALKV
ALIESOV
GAGTTFG
AAILLEIG

s 0;
TG 120
TG 247
GT 180
GT 307
GG 240
GG 367
TA 300

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Qy 961 GAGCGGGAAGACTCTCTGATTACTTCTGTAA 991
Db 1088 TACTCGGAAGACCCCTGATTATTTTGTGA 1118

RESULT 13
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DEFINITION Arabidopsis thaliana similar to protein phosphatase type 2A
ACCESSION AY093267
VERSION AY093267.1 GI:20259837
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1092)
REFERENCE Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,
Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,
Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
TITLE Submitted (26-MAR-2002) DNA Sequencing and Technology Center,

Stanford University, 855 California Avenue, Palo Alto,
USA
e-mail for correspondence: arab@sequence.stanford.edu
RIKEN Genomic Sciences Center (GSC) members carried
collection and clustering of RAFL cDNAs (RAFL cDNA :
Arabidopsis Full-length cDNA): Seki, M., Narusaka, M.
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members ca
sequencing and annotation of the RAFL cDNAs: Southwi
Nguyen, M., Karlin-Neumann, G., Lam, B., Miranda, M., P.
Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chu
Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shin
Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC)
equally to this work. Shinozaki, K. (RIKEN GSC) and
(SSP/Stanford) contributed equally to this work as ;
Location/Qualifiers

FEATURES

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gene

CDS

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ORIGIN

Query Match 42.0%; Score 573.8; DB 15; Length 1'
Best Local Similarity 76.4%; Pred. No. 1.5e-161;
Matches 704; Conservative 0; Mismatches 217; Indels

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	Matches 711;	Conservative 0;	Mismatches 229;	Indels	
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DB	348	GATGGAGTGCNAGCCG	TATCGGAAGCTGATGTGAAACTCTGTGTGATC		
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DB	408	TATACTTTGTTGAGGA	ATGGAATGTTCAACCGGTGAATGTCCGGTGACTC		
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QY	412	CCAGCAGACGAGGAGAT	TACGGAAGTATATGGTTCTATGATGAATGCC		
DB	648	TCATGAAGCCGGCAAA	TCACCCAGTGTATGGTTTTATGATGAATGCT		
QY	472	TGGAATGCGGAATGTT	TGGGAAGTACTTCACGATCTGTTTCGACTACCTGC		
DB	708	TGGCAATGCAAAATGT	TGGAAAGTATTTCCACTGATCTTTTGGATATCTAC		
QY	532	TCTCATTGAGCACGAGAT	TTTTTTGTCTTCATGGTGGTCTGTCTCCATCCG		
DB	768	ACTGATAGAGATCAGAT	ATTCTGTTGCATGGAGGACTCTCAACCTTCTC		
QY	592	AGATCAATCCGAGCCCT	AGATCGTATTCAGAAAGTGCAGGCGCAGAGGGCC		
DB	828	GGATAATATCCGAGCGCT	TGGACCGGTATACAAGAGGTTCCACATGAAGGGC		
QY	652	TCTACTCTGTCTGATCC	AGATGATCGTTGTGGATGGGGCATTTCCACCAAC		
DB	888	TCTCCTGTGGTCTGAT	CCAGATGATCGGTGTGGTTGGGGAAATCTCACCTC		
QY	712	TTTACTTTTTGGTCAAG	ATATTGCAGAGCAGGTTCAATCATACCAATGGT		

[illegible]

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 04:43:25 ; Search time 819 Seconds
(without alignments)
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Title: US-10-764-259-8

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Scoring table: IDENTITY_NUC

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Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	589.6	43.2	1386	10	ACC43349
5	584	42.8	1330	10	ACC43354
6	582.8	42.7	1298	10	ACC43351
7	579.6	42.5	1422	3	AAC46572
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21	514	37.7	1279	10	ACC43339	Acc4
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23	514	37.7	1531	10	ADD18470	Add1
24	512.4	37.5	1529	6	ABN95600	Abn9
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29	512.4	37.5	1541	14	ADX03728	Adxc
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31	510.2	37.4	1580	11	ADW22196	Adw2
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ALIGNMENTS

RESULT 1

ABN81332

ID ABN81332 standard; cDNA; 1365 BP.

XX AC ABN81332;

XX DT 02-SEP-2002 (first entry)

XX DE Physcomitrella patens PP2A-4 encoding cDNA SEQ ID NO 8.

XX KW Physcomitrella patens; PHSRP; phosphatase stress related pr
PP2C; enzyme; transgenic; plant; stress tolerance; gene; se

XX OS Physcomitrella patens.

XX FH Key Location/Qualifiers

XX CDS 71..991

XX FT /*tag= a

XX FT /product= "PP2A-4"

XX FN WO200246442-A2.

XX PD 13-JUN-2002.

XX PF 06-APR-2001; 2001WO-US011253.

XX PR 07-APR-2000; 2000US-0196001P.

XX PA (BADI) BASF PLANT SCI GMBH.

XX PI Da Costa E Silva, Bohnert HJ, Ishitani M, Van Thienen N

XX DR WPI; 2002-508562/54.

XX DR P-PSDB; ABH77578.

XX PT New transgenic plant cell transformed by phosphatase stress
protein coding nucleic acid whose expression in the cell re
increased tolerance to environmental stress compared to wil

XX PS Claim 18; Fig 2; 106pp; English.

XX CC The invention relates to a transgenic plant cell (I) transf

a

P2A;

R;

ell.

CC phosphatase stress-related protein (PHSRP) coding nucleic acid (ABN81330-
 CC ABN81334), where expression of the nucleic acid in the plant cell results
 CC in increased tolerance to an environmental stress as compared to a wild
 CC type variety of the plant cell. PHSRP encoding genes are useful for
 CC identifying Physcomitrella patens and related organisms, as markers for
 CC specific regions of the genome, mapping of genomes of organisms related
 CC to P. patens, identification and localisation of P. patens sequences of
 CC interest, evolutionary studies, determination of PHSRP regions required
 CC for function, modulation of a PHSRP activity, modulation of the
 CC metabolism of one or more cell functions, modulation of the transmembrane
 CC transport of one or more compounds and modulation of stress resistance.
 CC The gene is also useful for identifying and/or cloning PHSRP homologues
 CC in other cell types and organisms, for identifying an organism as being
 CC P. patens or its close relative and for evolutionary and protein
 CC structural studies. The present sequence is that of a PHSRP encoding
 CC polynucleotide of the invention
 XX

SQ Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;

Query Match 100.0%; Score 1365; DB 6; Length 1365;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 361 AGTGGCCCTGAAGTGGCGGTATAGGATAGGATCACAATCTTGGCGGGAACCAAGAG 420
 DB 361 AGTGGCCCTGAAGTGGCGGTATAGGATAGGATCACAATCTTGGCGGGAACCAAGAG 420
 QY 421 CAGGCGAGATTACGCAAGTATATGTTTCTATGATGAATGCCCTGCGAAGTATGAAATGC 480
 DB 421 CAGGCGAGATTACGCAAGTATATGTTTCTATGATGAATGCCCTGCGAAGTATGAAATGC 480
 QY 481 GAATGTTTGGAAAGTACTTCAACCGATCTGTTTCGACTACCTGCTCTGACAGCTCTCATTGA 540
 DB 481 GAATGTTTGGAAAGTACTTCAACCGATCTGTTTCGACTACCTGCTCTGACAGCTCTCATTGA 540
 QY 541 GCACGAGATTTTTTGTCTTCATGTTGGTGTCTGCTCCATCGCTCGACACATTAGATACAT 600
 DB 541 GCACGAGATTTTTTGTCTTCATGTTGGTGTCTGCTCCATCGCTCGACACATTAGATACAT 600
 QY 601 CCGAGCCCTAGATCGTATTCAAGAAAGTGCAGCAGAGGCGCGATGTGTGATCTACTCTG 660
 DB 601 CCGAGCCCTAGATCGTATTCAAGAAAGTGCAGCAGAGGCGCGATGTGTGATCTACTCTG 660
 QY 661 GTCTGATCCAGATGATCGTTTGGATGGGCAATTTCAACGAGGTGCGGTTTACTTTT 720
 DB 661 GTCTGATCCAGATGATCGTTTGGATGGGCAATTTCAACGAGGTGCGGTTTACTTTT 720
 QY 721 TGGTCAAGATATTGCAGAGCAGTCAATCATCAATGTTCTAAGTTTGGTTCGACGTGC 780

DB 721 TGGTCAAGATATTGCAGAGCAGTTCAATCATCAATCAATGTTCTAAAGTTTGG
 QY 781 TCACAGAGTTGTGATGGAAGATCAATTTGTTGTCAGGATAAAAATGTTG
 DB 781 TCACAGAGTTGTGATGGAAGATCAATTTGTTGTCAGGATAAAAATGTTG
 QY 841 CAGTGGCCCAATTTACTGTTTACCGCTGTGGGAAACATGGCCGCCATAATGG
 DB 841 CAGTGGCCCAATTTACTGTTTACCGCTGTGGGAAACATGGCCGCCATAATGG
 QY 901 AACATGAATCGGCTCTTTTCTTCAGTTTCAACACAGCACCGCGGCAAAAGTG
 DB 901 AACATGAATCGGCTCTTTTCTTCAGTTTCAACACAGCACCGCGGCAAAAGTG
 QY 961 GACGCGGAAGACTCCTGATTACTTTTCTGTAACATGGCCTATACATGTA
 DB 961 GACGCGGAAGACTCCTGATTACTTTTCTGTAACATGGCCTATACATGTA
 QY 1021 ACTGAATGTTTCTGTATAGTCACTTCCATCGAAGCAGTTTGGCCCTGAA
 DB 1021 ACTGAATGTTTCTGTATAGTCACTTCCATCGAAGCAGTTTGGCCCTGAA
 QY 1081 CCCTCATGATCTAGTAGTATGAAGTTATCTTTGAAAGTGTGTTGTTCCC
 DB 1081 CCCTCATGATCTAGTAGTATGAAGTTATCTTTGAAAGTGTGTTGTTCCC
 QY 1141 CTTGCTCCTCTGTTCAATTCATAAAAGTTGCCTTCAAGAACACTGAGATGTT
 DB 1141 CTTGCTCCTCTGTTCAATTCATAAAAGTTGCCTTCAAGAACACTGAGATGTT
 QY 1201 CTGCGACAGAGGAGCAGTGTCAATGTTGTCAGAGGTTTATAGTATTAGG
 DB 1201 CTGCGACAGAGGAGCAGTGTCAATGTTGTCAGAGGTTTATAGTATTAGG
 QY 1261 AGCAGTCTTACTTCAAAATCGATCAGAGACTTCTATGAAAAAGATGACGA
 DB 1261 AGCAGTCTTACTTCAAAATCGATCAGAGACTTCTATGAAAAAGATGACGA
 QY 1321 AACGTTCACTCCACACCTACTGTATATGTCATGTCGAGTCTGC 1365
 DB 1321 AACGTTCACTCCACACCTACTGTATATGTCATGTCGAGTCTGC 1365

RESULT 2

ABX16239
 ID ABX16239 standard; cDNA; 1365 BP.
 XX
 AC ABX16239;
 XX
 DT 08-APR-2003 (first entry)
 XX
 DE P. patens protein phosphatase PP2A-4 cDNA.
 XX
 KW Plant; ss; gene; PP2A-4; protein phosphatase; PHSRP; cold;
 KW phosphatase stress related protein; environmental stress; d;
 XX salt tolerance.
 XX
 OS Physcomitrella patens.
 XX
 FH Key Location/Qualifiers
 FT CDS 71..991
 FT /*tag= a
 FT /product= "PP2A-4"
 XX
 XX US2002152502-A1.
 PN 17-OCT-2002.
 XX
 XX 06-APR-2001; 2001US-00828302.
 XX
 XX 07-APR-2000; 2000US-0196001P.
 XX
 XX (SILV/) DA COSTA E SILVA O.

LC;

QY 97 GCAGATAGAGCAGCTGTCGGAGTGCAGCCGCTGTGCGAGTTGCGAGTCAAGAACTATG 156
 Db |||||
 QY 243 GCAGATCGCGAGCTGCGCATGCAAGTACTGCCGAGCGGAGGTCAAGCGCTCG 302
 Db |||||
 QY 157 TGATCAAGTCGCGAGCATCTTGGTGGAGAGTGGAACTGCGAGCCGCGAAGTGTCTGT 216
 Db |||||
 QY 303 CGAGCAGGCCAAGGCGCATCTTATGGAGAGTGGAACTGCGAGCCGCTGCGCTGTCTGT 362
 Db |||||
 QY 217 CACGTTTTCGGGTGATCATCGGCCAGTTTCTATGATCTCATCGAGCTTTCGCGCATAGG 276
 Db |||||
 QY 363 CACCGTCTGTGGCGACATCCAGCGCCAGTTCTATGACCTCATCGAGCTTTCGCGCATCGG 422
 Db |||||
 QY 277 AGCGAAGGCCCGCGACACGAACTACTTGTTCATGGCGGACTATGTGGATCGTGGATATTA 336
 Db |||||
 QY 423 CGCGACGCTCCCGACACCACTACTCTTCATGGCGGACTACGTGCGTACTGTTGCTACTA 482
 Db |||||
 QY 337 TTCTGTGAGATGTGTGCTCTTATGTGCGCTCTGAAAGTGGCGGTATAGGGATAGGATCAC 396
 Db |||||
 QY 483 TTCACTCGAAACAGTTTCTCTGTAGTGGCTTTGAAAGTCCGTTACAGAGATAGAATTAC 542
 Db |||||
 QY 397 ATCTTTCGGAGGGAACCGACGAGCAGGAGAGATTAAGCAAGTATATGTTTCTATGATGA 456
 Db |||||
 QY 543 AATACCTTAGAGGAATCATGAGAGCAGACAAATCACTCAAGTATATGGCTTCTATGATGA 602
 Db |||||
 QY 457 ATGCTTCGGAGTATGGAATGCGAACTGTTTGAAGTACTTTCAGGATCTGTTGCACTA 516
 Db |||||
 QY 603 ATGCTTAAGAAATATGGAATGCAATGCTCTGGAAGTATTTTACAGACTTGTGTTGATTT 662
 Db |||||
 QY 517 CCGTCTGAGACGTCTCAITGAGACGAGATTTTTTGTCTTCATGFGGTCTGTCTCC 576
 Db |||||
 QY 663 TTTGCTCTCTCAGCTCTTATAGAAAATCAGGCTCTCTGCTTTCATGTTGGCTCTCTCC 722
 Db |||||
 QY 577 ATCGCTCGACACATTAGATCATCGAGCCCTAGATGTTTCAAGAGTCCCGCAGCA 636
 Db |||||
 QY 723 GTCATGACGAGTGGATAATATTCGTTCTTGTATCGCGTACAGGAGTTCTCTCATGA 782
 Db |||||
 QY 637 GGGCCCGATGTGTGATCTACTCTGCTGATCCAGATGATCGTGTGGATGGGGCATTTTC 696
 Db |||||
 QY 783 AGGACCCATGTGTGATCTTTGTGCTGTGACCCAGATGACGATGGAATGGGGAATTTTC 842
 Db |||||
 QY 697 ACCAGAGTCCGCTTATACATTTTGGTCAAGATATTCAGAGCAGTTCATCATACCAA 756
 Db |||||
 QY 843 ACCAAGAGCAGCAGGTACACATTTGGGCAAGACATTCGCGAGCAGTTTCAACCAACAAA 902
 Db |||||
 QY 757 TGCTCTAAGTTTGGTTCACGCTGCTCACCGCTTGTGATGGAGGATACAAATGTGCGCA 816
 Db |||||
 QY 903 TGGTCTTCTCTCATTTCAAGGGCCCATCACTTGTGTAATGGAGGATTTAATTTGTGCGCA 962
 Db |||||
 QY 817 GGATAAAATGTGTACAGTTTTCAGTGGCCCAATTAAGTACCGTGTGGGGAACAT 876
 Db |||||
 QY 963 GGATAAAGATGTAGTACAGTCTTCAGTGGCTAACTATGTTTACCGCTGTGGTAACAT 1022
 Db |||||
 QY 877 GCGCCCAATAATGGAGATAGATGAACAATGAATCGGTCTTTTCTCAGTTTCGAACCCAGC 936
 Db |||||
 QY 1023 GCGTCTATCTTGAATTCGGGAAAAATGACCCAGAACTTCTTCAATTCGACCCCGC 1082
 Db |||||
 QY 937 ACCGCGCAAGTGAACAGATGTGACCGGAGACTCCTGATTAATTTCTGTAACATG 996
 Db |||||
 QY 1083 ACCTCGGCAATTTGAGCCAGACACAACTCGGAAAAACCCAGACTACTTTTGTGTAATTGTG 1142
 Db |||||
 QY 997 GCGTATACAT 1006
 Db |||||
 QY 1143 GTGGTGACAT 1152
 Db |||||

RESULT 8
 AAC44779
 ID AAC44779 standard; DNA; 1344 BP.
 XX
 AC AAC44779;
 XX
 DT 18-OCT-2000 (first entry)

XX Zea mays DNA fragment SEQ ID NO: 44101.
 DE Hybridisation assay; genetic mapping; gene expression contri
 XX protein identification; signal transduction pathway; metabo
 KW promoter; termination sequence; corn; ss.
 KW Zea mays subsp. mays.
 OS EP1033405-A2.
 XX 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-00301439.
 XX 25-FEB-1999; 99US-0121825P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 06-MAY-1999; 99US-0132487P.
 PR 07-MAY-1999; 99US-0132863P.
 PR 11-MAY-1999; 99US-0134256P.
 PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
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 PR 03-JUN-1999; 99US-0137528P.
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 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
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 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.

PR	21-JUN-1999;	99US-01398117P.	PR	27-AUG-1999;	99US-0151080P.	Query Match	42.2%;	Score 575.4;	DB 3;	Length 13.
PR	22-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-0151303P.	Best Local Similarity	75.2%;	Pred. No. 1.4e-168;		
PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151438P.	Matches 717;	Conservative	0;	Mismatches 236;	Indels
PR	23-JUN-1999;	99US-0140354P.	PR	01-SEP-1999;	99US-0151930P.	QY	45	CAGGGGGAGGCGAGAGTTGGGACAATGCCGTCTATGCGAGATGTAGACI	AG	104
PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.	DB	203	CGGGCGGGAGCGGGCGCGGACAGAGATGCCGTGCCACGGGGATCTGGACI	AG	262
PR	28-JUN-1999;	99US-0140821P.	PR	10-SEP-1999;	99US-0153070P.	QY	105	AGCAGCTCTCGGAGTGCAGCGGTTGTGCGGAGTTGGAGGTTGAAGAACTA	AG	164
PR	29-JUN-1999;	99US-0140991P.	PR	13-SEP-1999;	99US-0153758P.	DB	263	CGCAGCTCGGCGACTGCAAGTACCTGCCGAGGCGGAGGTCNAGTGCTC	AG	322
PR	30-JUN-1999;	99US-0141287P.	PR	15-SEP-1999;	99US-0154018P.	QY	165	CTCGGACGATCTTGGTGAGGAGTGGAAACGTGCGACGCCGTGAAGTGTCTT	TT	224
PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.	DB	323	CCAAGGCCATCTCATGGAGGAATGGAACGTGCGACGCCGTGCGCTGCCCT	TT	382
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.	QY	225	GCGGTGACATCCATGCCAGTTTTCATGATCTCATCGAGCTTTTCCGCATA	AG	284
PR	02-JUL-1999;	99US-0142053P.	PR	23-SEP-1999;	99US-0155139P.	DB	383	GCGGCGACATCCAGCGGCAGTTCTATGACCTCATCGAGCTCTTCCGCATC	TT	442
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.	QY	285	CGCCCCGACACCAACTACTTGTTCATGGGCGCACTATGTGGATCGTGGATAT	AG	344
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.	DB	443	CTCCCCGACACCAACTACTCTTTTCATGGCGCACTACGTGCACTCGTGGCTAT	AG	502
PR	09-JUL-1999;	99US-0142920P.								
PR	12-JUL-1999;	99US-0142977P.								
PR	13-JUL-1999;	99US-0143542P.								
PR	14-JUL-1999;	99US-0143624P.								
PR	15-JUL-1999;	99US-0144005P.								
PR	16-JUL-1999;	99US-0144085P.								
PR	19-JUL-1999;	99US-0144325P.								
PR	19-JUL-1999;	99US-0144331P.								
PR	19-JUL-1999;	99US-0144332P.								
PR	19-JUL-1999;	99US-0144333P.								
PR	19-JUL-1999;	99US-0144334P.								
PR	19-JUL-1999;	99US-0144335P.								
PR	20-JUL-1999;	99US-0144352P.								
PR	20-JUL-1999;	99US-0144632P.								
PR	20-JUL-1999;	99US-0144884P.								
PR	21-JUL-1999;	99US-0144814P.								
PR	21-JUL-1999;	99US-0145086P.								
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PR	22-JUL-1999;	99US-0145085P.								
PR	22-JUL-1999;	99US-0145087P.								
PR	22-JUL-1999;	99US-0145089P.								
PR	22-JUL-1999;	99US-0145192P.								
PR	23-JUL-1999;	99US-0145145P.								
PR	23-JUL-1999;	99US-0145218P.								
PR	23-JUL-1999;	99US-0145224P.								
PR	26-JUL-1999;	99US-0145276P.								
PR	27-JUL-1999;	99US-0145913P.								
PR	27-JUL-1999;	99US-0145918P.								
PR	27-JUL-1999;	99US-0145919P.								
PR	28-JUL-1999;	99US-0145951P.								
PR	02-AUG-1999;	99US-0146386P.								
PR	02-AUG-1999;	99US-0146388P.								
PR	02-AUG-1999;	99US-0146389P.								
PR	03-AUG-1999;	99US-0147038P.								
PR	04-AUG-1999;	99US-0147204P.								
PR	04-AUG-1999;	99US-0147302P.								
PR	05-AUG-1999;	99US-0147192P.								
PR	05-AUG-1999;	99US-0147260P.								
PR	06-AUG-1999;	99US-0147303P.								
PR	06-AUG-1999;	99US-0147416P.								
PR	09-AUG-1999;	99US-0147493P.								
PR	09-AUG-1999;	99US-0147935P.								
PR	10-AUG-1999;	99US-0148171P.								
PR	11-AUG-1999;	99US-0148319P.								
PR	12-AUG-1999;	99US-0148341P.								
PR	13-AUG-1999;	99US-0148565P.								
PR	13-AUG-1999;	99US-0148684P.								
PR	16-AUG-1999;	99US-0149368P.								
PR	17-AUG-1999;	99US-0149175P.								
PR	18-AUG-1999;	99US-0149426P.								
PR	20-AUG-1999;	99US-0149722P.								
PR	20-AUG-1999;	99US-0149723P.								
PR	20-AUG-1999;	99US-0149929P.								
PR	23-AUG-1999;	99US-0149902P.								
PR	23-AUG-1999;	99US-0149930P.								
PR	25-AUG-1999;	99US-0150566P.								
PR	26-AUG-1999;	99US-0150884P.								
PR	27-AUG-1999;	99US-0151065P.								
PR	27-AUG-1999;	99US-0151066P.								

QY	345	AGACTGTGTGCTCTTAGTGGCCCTGAAGTGGGTATAGGATAGGATCAAACTCTGC	404	PR	29-MAR-1999;	99US-0126785P.
Db	503	AAACGGTTCTCTGTAGTGACTTTGAAGTCCGTACAGATAGAAATACAACTACTTC	562	PR	01-APR-1999;	99US-0127462P.
QY	405	GAGGAAACACAGAGAGCGAGATTACGCAAGTATATGTTTCTATGATGAATCCCTGC	464	PR	06-APR-1999;	99US-0128234P.
Db	563	GAGGAAATCATGAGAGCAGACAAATCACTCAAGTGTACGGCTTCTATGATGAATGCTAA	622	PR	08-APR-1999;	99US-0128714P.
QY	465	GGAAGTATGGAATCGAATGTTTGGAACTCTTCCAGGATCTGTCGACTACCTGCCTC	524	PR	16-APR-1999;	99US-0129845P.
Db	623	GAAATATGGAATGCAATGATGGAAGTATTTACAGACTTGTGTATTTGCGCTC	682	PR	19-APR-1999;	99US-0130077P.
QY	525	TGACAGCTCTCATTTGAGCAGCAGATTTTGTCTTCACTGCTGCTCTCCATCGCTCG	584	PR	21-APR-1999;	99US-0130449P.
Db	683	TCACAGCTCTTATAGAAATCAGTCTCTCTTCACTGAGGCGCTCTCTCGTCAATGG	742	PR	23-APR-1999;	99US-0130510P.
QY	585	ACACATTAGATCAATCCGAGCCCTAGATCGTATTAAGAAAGTGGCGCAGGCGCCGA	644	PR	28-APR-1999;	99US-0130891P.
Db	743	ACACATTGGATAAATTCGTTCTCTTGATCGCATACAGAGGTACTCATGAAGACCCA	802	PR	30-APR-1999;	99US-0131449P.
QY	645	TGTGTGATCTACTCTGCTGCTGATCCAGATGATCGTGTGGATGGGGCATTTCAACACGAG	704	PR	30-APR-1999;	99US-0132048P.
Db	803	TGTGTGATCTTTTGTGGTCTGACCCAGATGACCGATGTGGGTGGGGAATTTCAACCCAGAG	862	PR	04-MAY-1999;	99US-0132407P.
QY	705	GTGCGGTTTACTTTTGGTCAAGATATTTGCGAGCAGTTCATATCATACCAATGGTCTAA	764	PR	05-MAY-1999;	99US-0132484P.
Db	863	GAGCAGGTTACACATTTGGCGAAGACATTTGCACAGAGTTCAACCATACAAATGCTCT	922	PR	06-MAY-1999;	99US-0132487P.
QY	765	GTGTTGGTGCAGTGCTCACAGCTTGTGATGGAAGGATACAAATTTGGTGGCAGGATAAAA	824	PR	07-MAY-1999;	99US-0132863P.
Db	923	CTCTCATTTCAAGGGCCCATCACTTTGTAATGGAAGGATTTAATTTGGTGGCAGGATAAGA	982	PR	11-MAY-1999;	99US-0134256P.
QY	825	ATGTTGTACAGTTTTCAGTCCCGCCCAATTAAGTACGGTGTGGGAACATGGCGGCCA	884	PR	14-MAY-1999;	99US-0134218P.
Db	983	ATGTAGTCACAGTCTTTCAGTGGCGCCCTAATTAAGTACGGTGTGGGAACATGGCGTCTA	1042	PR	14-MAY-1999;	99US-0134221P.
QY	885	TAATGGAGATAGATGAACAAATGAATCGTCTTTTTCAGTTCCAAACAGCAGCGCGGC	944	PR	18-MAY-1999;	99US-0134370P.
Db	1043	TTCTTGAATCGGGAACAAATGGACAGACTTCTTCAATTCACCCCGACCTCGGC	1102	PR	18-MAY-1999;	99US-0134768P.
QY	945	AAATGGAACCAAGTGTAGCGGGAAGAGCTCTGTATCTTTCTGTGTAACATGG	997	PR	19-MAY-1999;	99US-0134941P.
Db	1103	AAATTTGAGCCACACAACTCGCAAAACCCAGACTACTTTCTGTAAATTTGG	1155	PR	20-MAY-1999;	99US-0135124P.

RESULT 9
AAC43084
ID AAC43084 standard; DNA; 921 BP.
XX
AC AAC43084;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 37968.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
PR
PR 05-MAR-1999; 99US-0123180P.
PR
PR 09-MAR-1999; 99US-0123548P.
PR
PR 23-MAR-1999; 99US-0125788P.
PR
PR 25-MAR-1999; 99US-0126264P.

PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
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PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 05-AUG-1999; 99US-0147192P.
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PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
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PR 22-SEP-1999; 99US-0155139P.
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.

PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160814P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 42.0%; Score 573.8; DB 3; Length 92
Best Local Similarity 76.4%; Pred. No. 3.6e-168;
Matches 704; Conservative 0; Mismatches 217; Indels

QY 71 ATGCGTCATATGAGAGTGTAGACGGCAGATAGACGAGTGTGCGAGTG;
DB 1 ATGCGTGAACGGAGATCTGACCGTCAGATCGAGCAGTGTGCGAGTG;
QY 131 TCGGAGTTGGAGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGT;
DB 61 TCGGAGCGGATGTGAGGACGCTTTGCGATCAAGCAGAGCGATCCTTGT;
QY 191 AACGTGAGCCCGTGAAGTGTCTGTACGGTTTTCGGTGAATCCATGG;
DB 121 AATGTTACGCGGTGAAGTGTCTGTACCGTTTTCGGCGATATTCACGG;
QY 251 GATCTCATCGAGCTTTCCGCATAGGAGGCAAGCGCCGACACGAACTA;
DB 181 GACCTTATTGAGCTCTTTCGATCGGTGGCAACGCTCTCTGATCTACTA;
QY 311 GCGCACTATGTGGATCGTGGATATTTCTGTTCGAGACTGTGTCCCTCTT;
DB 241 GGAGACTATGTAGATCGTGGCTACTATTCACTAGAGACAGTTTCTCTATT;
QY 371 AAGTGGCGTATAGGATAGGATCACANTCTTTCGAGGAGAACCCAGAG;
DB 301 AAAGTGGCATACGGGATAGACTTACAACTCTTACGAGGGAATCACGAG;
QY 431 ACGCAAGTATATGTTTCTATGATGAATGCTCGGAAAGTATGGAATGCG;
DB 361 ACTCAAGTCTATGTTTATGACGAATGCTTGGAGAGTACGGAATGCG;
QY 491 AAGTACTTCACGGATCTGTTTCGACTACTGCTCTGACAGCTCTCATTTGA;
DB 421 AAGTATTTTACAGACCTTTTCGATTATCTTCTCTTACCGCCCTCATAGA;
QY 551 TTTTGTCTTCAATGTTGTTCTGTCTCCATCGCTCGACACATTAGATCATN;
DB 481 TTCTGTTTTCATGAGGGCTTTTCACCTTCTCTGGGATCTCTTGAATAAT;
QY 611 GATCGTATTCAAGAGTCCCGCAGAGGGCCCGGATGTGTGATCTACTCTG;
DB 541 GATCGATACAGGAGTTTCCACACGAAGGACCTATGTGTGATTTATTATG;

3 0;
NG 130
TA 60
AG 190
AT 120
AT 250
AT 180
AG 310
CG 240
CG 370
TA 300
TT 430
TT 360
AG 490
AG 420
TT 550
TT 480
TA 610
AG 540
TA 670
TT 600

OY	671	GATGATCGTTGGATGGGCAATTTCAACACGAGTGC	CGGTTTACTTTTGGTCAAGAT	730	PR	14-MAY-1999;	99US-0134221P.
Db	601	GATGATCGATGTGGATGGGAATATCTCCACGAGT	GCTGGTTATACATTTGGACAGGAT	660	PR	14-MAY-1999;	99US-0134370P.
OY	731	ATTGACGAGCAGTTCATATACCAATGCTTAAAGT	TGGTGGACGTGCTCACACGCTT	790	PR	18-MAY-1999;	99US-0134768P.
Db	661	ATCGCAGCTCAATTTAATCACAAATGGACTTAAG	TCTCATATCAAGAGCGCATCAACTT	720	PR	19-MAY-1999;	99US-0134941P.
OY	791	GTGATGGAAGGATACAAATTTGGTGCCAGGATAA	AAATGTTGTCACAGTTTTTCAGTCCCCC	850	PR	20-MAY-1999;	99US-0135124P.
Db	721	GTGATGGAAGGTTTAACTGGTGTGAGGATAAGAT	TGGTGACTGTGTTTAGTGACCA	780	PR	21-MAY-1999;	99US-0135353P.
OY	851	AATTAATCTGTTACCGTGTGGGAACATGCGCGCA	TAAATGGAGATAGATGAAACAATGAAT	910	PR	24-MAY-1999;	99US-0135629P.
Db	781	AACTATTGCTACCGGTGTGGAAACATGGCTGCCA	TTCTAGAGATAGGAGACATGGAG	840	PR	25-MAY-1999;	99US-0136021P.
OY	911	CGGCTTTTCTTCAGTTGGAACCAAGACCGCGGCA	AGTGAACCAAGATGTGACGCGGAAG	970	PR	27-MAY-1999;	99US-0136392P.
Db	841	CAAAACTTCTCCAGTTCCATCCAGTCTCCGACA	AGTTGMACTGTACTACTCGGAAG	900	PR	28-MAY-1999;	99US-0136782P.
OY	971	ACTCCTGATTACTTCTGTAA	991		PR	01-JUN-1999;	99US-0137222P.
Db	901	ACCCCTGATTATTTTGTGA	921		PR	03-JUN-1999;	99US-0137528P.
RESULT 10					PR	04-JUN-1999;	99US-0137502P.
AAC40149					PR	07-JUN-1999;	99US-0137724P.
ID	AAC40149 standard; DNA; 1267 BP.				PR	08-JUN-1999;	99US-0138094P.
XX	AAC40149;				PR	10-JUN-1999;	99US-0138540P.
AC					PR	10-JUN-1999;	99US-0138847P.
XX					PR	14-JUN-1999;	99US-0139119P.
XX					PR	16-JUN-1999;	99US-0139452P.
DT	17-OCT-2000 (first entry)				PR	16-JUN-1999;	99US-0139453P.
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 27232.				PR	17-JUN-1999;	99US-0139492P.
KW	Hybridisation assay; genetic mapping; gene expression control;				PR	18-JUN-1999;	99US-0139454P.
KW	protein identification; signal transduction pathway; metabolic pathway;				PR	18-JUN-1999;	99US-0139455P.
KW	promoter; termination sequence; ss.				PR	18-JUN-1999;	99US-0139457P.
XX	Arabidopsis thaliana.				PR	18-JUN-1999;	99US-0139458P.
OS					PR	18-JUN-1999;	99US-0139459P.
XX					PR	18-JUN-1999;	99US-0139460P.
PN	EP1033405-A2.				PR	18-JUN-1999;	99US-0139461P.
XX					PR	18-JUN-1999;	99US-0139462P.
PD	06-SEP-2000.				PR	18-JUN-1999;	99US-0139463P.
XX					PR	18-JUN-1999;	99US-0139750P.
PF	25-FEB-2000; 2000EP-00301439.				PR	18-JUN-1999;	99US-0139763P.
XX					PR	21-JUN-1999;	99US-0139817P.
PR					PR	22-JUN-1999;	99US-0139899P.
PR					PR	23-JUN-1999;	99US-0140353P.
PR					PR	23-JUN-1999;	99US-0140354P.
PR					PR	24-JUN-1999;	99US-0140695P.
PR					PR	28-JUN-1999;	99US-0140823P.
PR					PR	29-JUN-1999;	99US-0140991P.
PR					PR	30-JUN-1999;	99US-0141287P.
PR					PR	01-JUL-1999;	99US-0141842P.
PR					PR	01-JUL-1999;	99US-0142154P.
PR					PR	02-JUL-1999;	99US-0142055P.
PR					PR	06-JUL-1999;	99US-0142390P.
PR					PR	08-JUL-1999;	99US-0142803P.
PR					PR	09-JUL-1999;	99US-0142920P.
PR					PR	12-JUL-1999;	99US-0142977P.
PR					PR	13-JUL-1999;	99US-0143542P.
PR					PR	14-JUL-1999;	99US-0143624P.
PR					PR	15-JUL-1999;	99US-0144005P.
PR					PR	16-JUL-1999;	99US-0144085P.
PR					PR	16-JUL-1999;	99US-0144086P.
PR					PR	19-JUL-1999;	99US-0144331P.
PR					PR	19-JUL-1999;	99US-0144332P.
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PR					PR	20-JUL-1999;	99US-0144352P.
PR					PR	20-JUL-1999;	99US-0144632P.
PR					PR	20-JUL-1999;	99US-0144884P.
PR					PR	21-JUL-1999;	99US-0144814P.
PR					PR	21-JUL-1999;	99US-0145086P.
PR					PR	21-JUL-1999;	99US-0145088P.
PR					PR	22-JUL-1999;	99US-0145085P.
PR					PR	22-JUL-1999;	99US-0145087P.
PR					PR	22-JUL-1999;	99US-0145089P.
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PR					PR	23-JUL-1999;	99US-0145218P.
PR					PR	23-JUL-1999;	99US-0145224P.
PR					PR	26-JUL-1999;	99US-0145276P.

PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147302P.	Query Match 41.1%; Score 561; DB 3; Length 1267		
PR	05-AUG-1999;	99US-0147192P.	Best Local Similarity 75.6%; Pred. No. 4.4e-164;		
PR	05-AUG-1999;	99US-0147260P.	Matches 696; Conservative 0; Mismatches 225; Indels		
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147493P.	Qy	71	ATGCCGTATATGCAGATGTAGACCGGCAGATAGACAGCTGTGCGAGTG;
PR	09-AUG-1999;	99US-0147935P.	Db	159	ATGCCGTCAACCGGAGATCTCGACCGTCAGATCGAACAGCTAAATGAGTG;
PR	10-AUG-1999;	99US-0148171P.	Qy	131	TCGGAGTTGGAGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGT;
PR	11-AUG-1999;	99US-0148319P.	Db	219	GGTGAAGCAGACGTGAAGATCCITTTGGGATCAAGCTAAAGCGATTTCTCGT;
PR	12-AUG-1999;	99US-0148341P.	Qy	191	AACGTGCAGCCCGTGAAGTGTCTGTCAACGGTTTTCGGTGCACATCCATGG;
PR	13-AUG-1999;	99US-0148565P.	Db	279	AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATGCGCGATATCCATGG;
PR	16-AUG-1999;	99US-0149368P.	Qy	251	GATCTCATCGAGCTTTTCCGCATAGGAGCGCAAGCGCCCGACACGAACTA;
PR	17-AUG-1999;	99US-0149175P.	Db	339	GACCTAATTGAGCTATTTCGTATTGGTGAATGCTCTCTGATACTAATTA;
PR	18-AUG-1999;	99US-0149426P.	Qy	311	GGCGACTATGGGATCGTGGATATATTTCTGTGAGACTGTGTGCTCTTT;
PR	20-AUG-1999;	99US-0149722P.	Db	399	GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTATT;
PR	20-AUG-1999;	99US-0149723P.	Qy	371	AAGGTGCGGTATAGGATAGGATCACAATCTTGCAGAGGAAACCGAGAG;
PR	20-AUG-1999;	99US-0149929P.	Db	459	AAGGTGCGTTACAGGCACAGACTTACGATCTCGGAGGGGATCATGAGAG;
PR	23-AUG-1999;	99US-0149902P.	Qy	431	ACGCAAGTATATGGTTTCTATGATGAATGCTCGGGAAGTATGGAAATGCI;
PR	23-AUG-1999;	99US-0149930P.	Db	519	ACACAAGTCTATGGTTTTTATGACGAATGCTTGAGGAATACGGAAATGC;
PR	25-AUG-1999;	99US-0150566P.	Qy	491	AAGTACTTCAGGATCTGTTGCACTACTGCTGCTGACAGCTCTCATTTG;
PR	26-AUG-1999;	99US-0150884P.	Db	579	AAGTATTTTACGGACCTTTTCGATTAICTCCCTCTAACAGCACTCATAGA;
PR	27-AUG-1999;	99US-0151065P.	Qy	551	TTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACACATTAGATCACAT;
PR	27-AUG-1999;	99US-0151066P.	Db	639	TTCTGTTTGCATGGAGGCTTTTCACCTTCTCTGGATACTCTTGACAAATAT;
PR	30-AUG-1999;	99US-0151303P.	Qy	611	GATCGTATTCAAGAAGTGCCGACAGAGGCCCGGATGTGTGATCTACTCTG;
PR	31-AUG-1999;	99US-0151438P.	Db	699	GATCGAATACAAGAGGTTCCACACAGGAAGCAATGTGCGATCTACTCTG;
PR	01-SEP-1999;	99US-0151930P.	Qy	671	GATGATCGTGTGGATGGGCAATTTCCACCAGAGTGCCGGTTATACTTTT;
PR	07-SEP-1999;	99US-0152363P.	Db	759	GACGATCGTGTGGATGGGGAATATCTCCTCGTGTGCTGGTTACACGTT;
PR	10-SEP-1999;	99US-0153070P.	Qy	731	ATTGCAGAGCAGTTCATATCATACCAATGGTCTTAAGTTTGGTTGCACTGTC;
PR	13-SEP-1999;	99US-0153758P.	Db	819	ATTGCTACTAGTTCAATCATAAACATGGAATGAGTCTGATATCAAGAGCI;
PR	15-SEP-1999;	99US-0154018P.	Qy	791	GTGATGGAAGGATACATTTGGTGGCAGGATAAAATGTTGTCAAGTTTTT;
PR	16-SEP-1999;	99US-0154039P.	Db	879	GTAATGGAAGGCTATAATTGGTGTGAGGAAAGAACGTAAGTGCACAGTGT;
PR	20-SEP-1999;	99US-0154779P.	Qy	851	AATTACTGTTACCCCTGTGGGAACATGCCGCCATAATGGAGATAGATGA;
PR	22-SEP-1999;	99US-0155133P.	Db	939	AACCTACTGTTACAGATGTGGAACATATGCCCCCAATTTCTTGAGATGGAGA;
PR	23-SEP-1999;	99US-0155486P.	Qy	911	CGGTCTTTTTCAGTTCGAACCCAGCACCGCGGCAAGTGAACCAAGATGT;
PR	24-SEP-1999;	99US-0156459P.	Db	999	CAGAACTTCTTCAATTCGATCCAGACCTTAGACAAGTCGAACCGGATAC;
PR	29-SEP-1999;	99US-0156596P.			
PR	04-OCT-1999;	99US-0157117P.			
PR	05-OCT-1999;	99US-0157753P.			
PR	06-OCT-1999;	99US-0157865P.			
PR	07-OCT-1999;	99US-0158029P.			
PR	08-OCT-1999;	99US-0158232P.			
PR	12-OCT-1999;	99US-0158369P.			
PR	13-OCT-1999;	99US-0159293P.			
PR	13-OCT-1999;	99US-0159294P.			
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PR	14-OCT-1999;	99US-0159329P.			
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PR	21-OCT-1999;	99US-0160767P.			
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PR	21-OCT-1999;	99US-0160815P.			
PR	22-OCT-1999;	99US-0160980P.			
PR	22-OCT-1999;	99US-0160981P.			
PR	22-OCT-1999;	99US-0160989P.			
PR	25-OCT-1999;	99US-0161404P.			

QY 971 ACTCCTGATTACTTCTGTAA 991
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Db 1059 ACCCTGATTATTTTGTGA 1079

RESULT 11
AAC43368
ID AAC43368 standard; DNA; 921 BP.
XX
AC AAC43368;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 39005.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
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PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
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PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.

PR	13-AUG-1999;	99US-0148684P.	
PR	16-AUG-1999;	99US-0149368P.	
PR	17-AUG-1999;	99US-0149175P.	
PR	18-AUG-1999;	99US-0149426P.	
PR	20-AUG-1999;	99US-0149722P.	
PR	20-AUG-1999;	99US-0149723P.	
PR	20-AUG-1999;	99US-0149923P.	
PR	23-AUG-1999;	99US-0149902P.	
PR	23-AUG-1999;	99US-0149930P.	
PR	25-AUG-1999;	99US-0150566P.	
PR	26-AUG-1999;	99US-0150884P.	
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PR	30-AUG-1999;	99US-0151303P.	
PR	31-AUG-1999;	99US-0151438P.	
PR	01-SEP-1999;	99US-0151930P.	
PR	07-SEP-1999;	99US-0152363P.	
PR	10-SEP-1999;	99US-0153070P.	
PR	13-SEP-1999;	99US-0153758P.	
PR	15-SEP-1999;	99US-0154018P.	
PR	16-SEP-1999;	99US-0154039P.	
PR	20-SEP-1999;	99US-0154779P.	
PR	22-SEP-1999;	99US-0155139P.	
PR	23-SEP-1999;	99US-0155488P.	
PR	24-SEP-1999;	99US-0155659P.	
PR	28-SEP-1999;	99US-0156458P.	
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PR	22-OCT-1999;	99US-0160981P.	
PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
PR	25-OCT-1999;	99US-0161405P.	
PR	25-OCT-1999;	99US-0161408P.	
PR	26-OCT-1999;	99US-0161359P.	
PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161361P.	
PR	28-OCT-1999;	99US-0161920P.	
PR	28-OCT-1999;	99US-0161992P.	
PR	28-OCT-1999;	99US-0161993P.	
PR	29-OCT-1999;	99US-0162142P.	

Query Match 41.0%; Score 559.4; DB 3; Length 921;
Best Local Similarity 75.5%; Pred. No. 1.2e-163;
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY	71	ATGCCGTGATATGCAGATGTAGACCGGAGATAGACGAGCTTCGGAGTGCAGCGGTTG	130
DB	1	ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTGTAAAGCCGTTA	60
QY	131	TCGGAGTTGGAGTGCAAGAACCTATGTATCAAGCTCGGACGATCTGTGTGGAGGATGG	190

Db	61	GGTGAAGCAGACGCTGAAGATCCTTTGGCATCAAGCTAAAGCGATCTCTGT	120
QY	191	AACGTGCAGCCCGTGAAGTGTCTGTACCGTTTTGCGGTGACATCCATGG	250
Db	121	AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATGCGGCGATATCCATGG	180
QY	251	GATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGCCGACACGAACTA	310
Db	181	GACCTAATTGAGCTATTTCGTAITGGTGGTAATGCTCTGTATCTAAATTA	240
QY	311	GGCGACTATGTGGATCGTGATATATTCTCTCGAGACTGTGTGCTCTT	370
Db	241	GGAGATTATGTAGATCGTGGCTACTATTCTCTAGAAAACAGTCTCTCTATT	300
QY	371	AAGTGGCGGTATAGGATPAGGATCACAATCTTGGAGGAAACCGAGAG	430
Db	301	AAGTGGCGTTACAGGACAGACTTACGATCCTCGGAGGGAATCATGAGAG	360
QY	431	ACGCAAGTATATGTTTCTATGATGAATGCCCTCGGAAGTATGGAAATGC	490
Db	361	ACACAAGTCTATGTTTATATGACGAATGCTTGAGGAAATACGGAATGCG	420
QY	491	AAGTACTTCAAGGATCTGTTCCGACTACCTGCTCTGACAGCTCTCATTTGA	550
Db	421	AAGTATTTTACGGACCTTTTCGATTTATCTCCTCTTACAGCACTCATAGA	480
QY	551	TTTTGTCTTCAATGTTGTTCTCTCCATCGCTGCTGCACACATTAGATCAAT	610
Db	481	TTCTGTTTGGCATGAGGCTTTTCACTTCTCTGGATACTCTTGTGACAAAT	540
QY	611	GATCGTATTCAAGAGTCCCGCAGGCGGCGGATGTGTGATCTACTCTG	670
Db	541	GATCGAATACAAAGAGTTTCCACACGAAGGACCAATGTGCGATCTACTCTG	600
QY	671	GATGATCGTTGCGATGGGCAATTTCAACGAGGTGCGGTTTATACTTTT	730
Db	601	GACGATCGTTGTGATGGGGAATATCTCTCTGTTGCTGGTTACACGTT	660
QY	731	ATTGCAGACGAGTTCAATCATACCAATGGTCTAAAGTTTGGTTGCAACGTGC	790
Db	661	ATTGCTACTCAGTTTAAATCATAAACAATGGAATGAGTCTGATCTCAAGAGC	720
QY	791	GTGATGGAGGATACAAATGTGTGCGAGGATAAAATGTTGTACAGTTTTT	850
Db	721	GTAATGGAAGCTATAATTGTTGTGAGGAAAGAACGTAAGTACAGTGT	780
QY	851	AATTACTGTTTACCGCTGTGGGAACATGGCCGCCATAAATGGAGATAGATGA	910
Db	781	AATTACTGTTTACAGATGTGGAAAACATGSCCGCAATTTCTTGAGATTGGAGA	840
QY	911	CGGTCTTTTCTTCAAGTTCGAACCGACACCGCGGCAAGTGAACCGAGATGT	970
Db	841	CAGAACTTCTTCAATTCGATCCAGCACCTAGACAAAGTCGAACCCGATAC	900
QY	971	ACTCCTGATTACTTCTGTAA	991
Db	901	ACCCCTGATTATTTTGTGA	921
RESULT 12			
ID	ABZ12900	standard; DNA; 921 BP.	
XX	AC	ABZ12900;	
XX	DT	21-JAN-2003 (first entry)	
XX	DE	Arabidopsis thaliana stress regulated gene SEQ ID NO 705.	
XX	KW	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	
XX	OS	Arabidopsis thaliana.	
XX	XX		

PN WO200216655-A2.
XX 28-FEB-2002.
XX 24-AUG-2001; 2001WO-US026685.
XX 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX (Scripps) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
DR WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 144; SEQ ID NO 705; 577pp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 921 BP; 252 A; 183 C; 225 G; 261 T; 0 U; 0 Other;

Query Match 41.0%; Score 559.4; DB 6; Length 921;
Best Local Similarity 75.5%; Pred. No. 1.2e-163;
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

71 ATGCGGTATATGAGATGTTAGACCGGAGATAGAGAGAGTGTGCGAGTGCAAGCGTTG 130
1 ATGCGGTTAAACGGAGATCTGACCGTCCAGATCGAAGAGTAAATGAGTAAAGCGTTA 60
131 TCGGAGTTGGAGTGAAGAACTATGTATCAAGCTCGGAGATCTTGGTGGAGAGTGG 190
61 GGTGAAGCAGACGTGAAGATCCTTTGCGATCAAGCTAAAGCGATTCTTTGTTGAGGAATAT 120
191 AACGTGCAAGCGGTGAAGTGTCTCTCAAGTTTGGGTGATCCATCGCCAGTTTCAT 250
121 AATGTTCAACCGGTTAAGTGTCCGGTATCGGTATCGCGGATATCCATGCGCCAGTTTAT 180
251 GATCTCATGAGCTTTTCCGATAGGAGGCAAGCGCCCGACACGAACTACTTTGTTCAATG 310
181 GACCTAATGAGCTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240
311 GCGGCTATGTGGATCGTGGATATTTATTTCTGTCGAGATGTGTGCTCTTAGTGCCCGT 370
241 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTATTTGTTGTCATTA 300
371 AAGTGGCGGTATAGGATAGGATCAATCTTGGAGGGAACCCAGAGAGCGGAGATT 430
301 AAGTGGCGGTATAGGATAGGATCAATCTTGGAGGGAACCCAGAGAGCGGAGATT 360
431 ACGCAAGTATATGTTTCTTATGATGAATGCTCGGAGAGTATGGAATGCGAATGTTGG 490
361 ACACAAGTCTATGTTTATGACGAATGCTTGGAGGAATACGGAATGCAATGTGTTGG 420
491 AAGTACTTCAAGGATCTGTTGAGTCTTCTGAGAGTCTCTTAGGACGAGATT 550
421 AAGTATTTTACGAGCTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGATCAGGTT 480

QY 551 TTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACACATTAGATCAAT 610
DB 481 TTCTGTTGCAATGAGGCGCTTTTCACTTCTCTGGATCTCTTGCAATAT 540
QY 611 GATCGTATTTCAAGAAGTGGCCGACAGAGGCGCGATGTGTGATCTACTCTG 670
DB 541 GATCGAATACAAAGAGTTTCCACAGGAAGGACCAATGTGCGATCTACTCTG 600
QY 671 GATGATCGTTCGTGATGGGCAATTTTCAACCAAGAGTGGCGGTTTACTTT 730
DB 601 GACGATCGTTCGTGATGGGGAATATCTCTCTGTTGTTGTTGTTGTTGTT 660
QY 731 ATTGCAGAGCAGTTTCAATCATACCAATGGTCTTAAAGTTTGGTTGCAAGTTC 790
DB 661 ATTGCTACTCAGTTTAAATCAATAAATGAGTCTGAGTCTGATCTCAAGAGC 720
QY 791 GTGATGAGGATACAAATTTGTTGCGAGGATTTAAATGTTGTTGTTGTTGTT 850
DB 721 GTAATGGAAGGCTATAATTTGGTGTGAGGAAAGAACGTTAGTGACAGTGT 780
QY 851 AATTACTGTTCACCGCTGTGGGAACATGCGCCCATTAATGGAGATAGATGA 910
DB 781 AACTACTGTTCACAGATGTGGAAACATGCGCCCAATTTCTTGAGATTGGAGA 840
QY 911 CGGTCTTTTCTTCAGTTTCGAACACCGGCGGCAAAAGTGAACCAAGATGT 970
DB 841 CAGAACTTCTTCAATTCGATCCAGCACCTAGACAAAGTGAACCGGATAC 900
QY 971 ACTCTGTGATTTACTTTCTGTAA 991
DB 901 ACCCTGATTTATTTTGTGA 921

RESULT 13
ACC43342
ID ACC43342 standard; cDNA; 1243 BP.
XX AC ACC43342;
XX AC ACC43342;
DT 11-AUG-2003 (first entry)
XX
DE Protein phosphatase stress-related polypeptide BnPP2A-1 cDN
XX
KW Protein phosphatase stress-related polypeptide; PPSRP; PpPE
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OSpP2A-2; OSpP2A-3; plant tolerance; environmental stress;
KW drought; salinity; cold; enzyme; gene; ss.
XX
OS Brassica napus.
XX
FH Key Location/Qualifiers
FT CDS 150..1070
FT /*tag= a
FT /product= "protein phosphatase stress-relat
FT polypeptide"
XX
FN WO2003020914-A2.
XX
PD 13-MAR-2003.
XX
PF 05-SEP-2002; 2002WO-US028445.
XX
PR 05-SEP-2001; 2001US-0317305P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Bohnert HJ, Chen R, Ishitani M, Van Thiel N, Da Costa
XX
DR WPI; 2003-300886/29.
DR P-PSDB; ABP98027.
XX
PT New protein phosphatase stress-related polypeptide coding r
cid, cid, such
useful for modulating plant's tolerance to an environmental

as drought, increased salinity and cold.

Claim 1; Page 74-75; 107pp; English.

The present sequence encodes a protein phosphatase stress-related polypeptide (PPSRP). The specification describes PPSRP polypeptides designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1, GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP polypeptides and polynucleotides are useful for modulating plant tolerance to an environmental stress such as drought or increased salinity and cold. They are also useful in identification and localization of Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa and related organisms, mapping of genomes of organisms related to the above species, in a evolutionary and polypeptide structural studies, in determination of PPSRP regions required for function, modulation of PPSRP activity, modulation of metabolism of one or more cell functions and transmembrane transport of one or more components

Sequence 1243 BP; 337 A; 258 C; 299 G; 349 T; 0 U; 0 Other;

Query Match	40.5%;	Score 552.8;	DB 10;	Length 1243;
Best Local Similarity	74.6%;	Pred. No. 1.6e-161;		
Matches 695;	Conservative 0;	Mismatches 237;	Indels 0;	Gaps 0;
Qy	60	AGGTTGGACAAATGCGTCATATGATGAGATGATGACCGGACAGATGAGCGAGTTCGGAGT	119	
Db	139	AGGAGAGACGATGCGGAGACGGGAGACATCGATCGTCAGATCGAGCAGCTGATGGAAT	198	
Qy	120	GCAAGCGTTCGCGAGTTCGAGGTGAGACCACTTATGTATCAAGCTCGGACGATCTGG	179	
Db	199	GTAAGCGTTCGCGAGCGGAGGTGAAGACGCTGTGCGAGCAAGCGAGGCGGATCTGG	258	
Qy	180	TGGAGGAGTGAACCTGCGAGCGGTCGAGTGTCTGTCACCGTTCGCGTGCATCCATG	239	
Db	259	TGGAGGAGTGAAGTTCGAGCGGTAAAGTGTCCGTCACCGTTCGCGGACATCCACG	318	
Qy	240	GCCAGTTTCATGATCTCATCGAGCTTTTCCGCATAGGAGCAAGCGCCCGACACGAAT	299	
Db	319	GCCAGTTTACGATCTGATTCGAGCTTTTAAAGATCGGTGGTCTTCGCGCTGACACCAAT	378	
Qy	300	ACTTGTTCATCGGCGACTATCGGATCGTGATATTCTGTCGAGACTGTGCGTCT	359	
Db	379	ATCTCTTCATGGGCGATTACGTAGATCGAGGGTATTATCTGTGGAGACAGTCTCGCTCT	438	
Qy	360	TAGTGGCCCTGAAGTGGGTATAGGGATAGGATCACAAATCTTGGAGGGAACCAACGAGA	419	
Db	439	TGGTAGCACTCAAGTTCGCTACAGAGATAGGCTTACCATCTTAAGAGGGATCACGAA	498	
Qy	420	GCAGCAGATTACGCAAGTATATGTTTCTATGATGAATGCTCGGGAAGTATGGAATG	479	
Db	499	GCCGCCAAATTTACTCAAGTGTATGGATTTATGATGAGTGTGAGAAAATATGGAATG	558	
Qy	480	CGAATGTTTGAAGTACTTCAAGGATCTGTCGACTACCTGCTGACAGCTCTCATTTG	539	
Db	559	CTAATGTCGGAACACCTTCACTAGACCTTTTGGATTATCTTCCTCTTACAGCTCTCATCG	618	
Qy	540	AGCACGAGATTTTGTCTTCTCATGTGTGCTGTCTCCATCGCTGCACACATTAGATCACA	599	
Db	619	AGAGTCAGTTTCTGTTTACATGAGGGGCTCTCACCTTCTTTAGATACATTTGACACA	678	
Qy	600	TCCGAGCCCTAGATCGTATTCGAAGGATGCGCGACAGGGCCGATGTGTATCTTACTCT	659	
Db	679	TCCGTTCTTAGATCGAATCCAAGAGGTTCCACATGAAGGACCTATGTGTATCTGTTAT	738	
Qy	660	GGTCTGATCCAGATGATCGTTGTGATGGGCAATTTACACAGAGTCCCGTTATATCTT	719	
Db	739	GGTCCGATCCAGATGATCGATCGCGTTGGGGAATATCTCCTCGTGGCGCAGGCTACAGT	798	
Qy	720	TGTGTCAGATATTCGACAGCAGGTTCAATCATACATACCAATGGTCTAAGTTTGGTTCACCGTG	779	
Db	799	TCGGACAGATATCGCTACTCAGTTTAAACCAACCACTGAGTCTGATCTCAAGAG	858	

Qy	780	CTACACGCTTGTGATGGAAGGATACAAATTTGGTCCCGAGGATAAAAAATGTTT	839	
Db	859	CACACCAACTTGTTCATGGAAGGTTTATAATTTGGTCCCAAGAAAGAACGTTT	918	
Qy	840	TCAGTGGCCCCCAATTTACTGTTTACCGCTGTGGGAACATGGCCGCCATAATG	899	
Db	919	TTAGCGCCCCAAACTATTGTTACCGATGCGGCAACATGGCTGCTATTCTTA	978	
Qy	900	AAACAATCAATCGGTCCTTTTTCAGTTTCGAACCGACACCGCCGCAAAAGT	959	
Db	979	AGAACATGGACCAACAACTTCTCTTCAGTTTCGATCCAGCCGCCACGTCACAGTA	1038	
Qy	960	TGACGCGGAAGACTCTCTGATTAATCTTTCTGTAA	991	
Db	1039	CTACACGCAAAATCCAGATTACTTTTTGTAA	1070	
RESULT 14				
AAC45630				
ID	AAC45630 standard; DNA; 1259 BP.			
XX	AAC45630;			
AC	AAC45630;			
XX	18-OCT-2000 (first entry)			
DT	Arabidopsis thaliana DNA fragment SEQ ID NO: 47194.			
XX	Hybridisation assay; genetic mapping; gene expression contr;			
DE	protein identification; signal transduction pathway; metabo			
KW	promoter; termination sequence; ss.			
KW	Arabidopsis thaliana.			
XX	EP1033405-A2.			
XX	06-SEP-2000.			
XX	25-FEB-2000; 2000EP-00301439.			
XX	25-FEB-1999; 99US-0121825P.			
PR	05-MAR-1999; 99US-0123180P.			
PR	09-MAR-1999; 99US-0123548P.			
PR	23-MAR-1999; 99US-0125788P.			
PR	29-MAR-1999; 99US-0126264P.			
PR	01-APR-1999; 99US-0126785P.			
PR	06-APR-1999; 99US-0127462P.			
PR	08-APR-1999; 99US-0128234P.			
PR	16-APR-1999; 99US-0128714P.			
PR	19-APR-1999; 99US-0129845P.			
PR	21-APR-1999; 99US-0130077P.			
PR	23-APR-1999; 99US-0130449P.			
PR	23-APR-1999; 99US-0130510P.			
PR	28-APR-1999; 99US-0130891P.			
PR	30-APR-1999; 99US-0131449P.			
PR	30-APR-1999; 99US-0132048P.			
PR	04-MAY-1999; 99US-0132407P.			
PR	05-MAY-1999; 99US-0132484P.			
PR	06-MAY-1999; 99US-0132485P.			
PR	06-MAY-1999; 99US-0132486P.			
PR	07-MAY-1999; 99US-0132487P.			
PR	11-MAY-1999; 99US-0132863P.			
PR	14-MAY-1999; 99US-0134218P.			
PR	14-MAY-1999; 99US-0134219P.			
PR	14-MAY-1999; 99US-0134221P.			
PR	14-MAY-1999; 99US-0134370P.			
PR	18-MAY-1999; 99US-0134768P.			
PR	19-MAY-1999; 99US-0134941P.			
PR	20-MAY-1999; 99US-0135124P.			
PR	21-MAY-1999; 99US-0135353P.			
PR	24-MAY-1999; 99US-0135629P.			
PR	25-MAY-1999; 99US-0136021P.			

PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
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PR 19-JUL-1999; 99US-0144323P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
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PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
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PR 23-JUL-1999; 99US-0145145P.
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PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 02-AUG-1999; 99US-0146386P.
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PR 13-AUG-1999; 99US-0148565P.
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PR 04-OCT-1999; 99US-0157117P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 28-OCT-1999; 99US-0161993P.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 06:03:11 ; Search time 5144 seconds
(without alignments)
12415.313 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: gb_est2:*
- 3: gb_est3:*
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- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
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- 9: gb_gss1:*
- 10: gb_gss2:*
- 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	738.4	54.1	740	3	BJ598448
C 3	736.8	54.0	752	3	BJ591074
C 4	734.8	53.8	762	3	BJ976562
C 5	697.8	51.1	706	3	BJ585338
C 6	680.4	49.8	706	3	BJ599008
C 7	653	47.8	666	3	BJ503182
C 8	576.2	42.2	1429	4	AY104802
C 9	575.4	42.2	921	10	CL964875
C 10	574.2	42.1	1283	4	CNS0ADRX
C 11	571	41.8	1285	4	CNS0AD99
C 12	564.6	41.4	1278	4	CNS0ADNP
C 13	556.6	40.8	1534	4	AY108657
C 14	556.2	40.7	1250	4	CNS0ADL7
C 15	520.2	38.1	849	7	CO082158
C 16	516.6	37.8	1586	4	AY609732
C 17	515.6	37.8	1723	4	CR624064
C 18	513.8	37.6	933	7	CV291986
C 19	507.8	37.2	906	7	CR278240
C 20	504.8	37.0	797	8	DR683092
C 21	504.2	36.9	1371	4	CNS0A3F1
C 22	503.6	36.9	1749	4	CR594899

23	503.6	36.9	1758	4	CR624778
24	503.6	36.9	1781	4	CR596427
25	503.6	36.9	1830	4	CR619537
26	500.4	36.7	1983	4	AY609733
27	499.8	36.6	1718	4	AY104886
28	499.6	36.6	901	4	CNS0ADBG
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30	496	36.3	972	8	DR558418
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35	487	35.7	1016	5	BU901162
36	486.2	35.6	1430	4	CR611096
37	484.6	35.5	763	1	AJ803648
38	484.4	35.5	923	1	AM011553
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41	479.8	35.2	884	5	BU192665
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ALIGNMENTS

RESULT 1
BJ587709/c

LOCUS

DEFINITION

BJ587709 746 bp mRNA linear
BJ587709 normalized full length cDNA library, chloro
caulonemata and malformed buds Physcomitrella patens
cDNA clone pbbh34c10 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

T-2003
patens

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a.

i,K.,

plant

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738 AGCAGTTCATCATACCAATGCTTAAGTTGGTTCACGCTCTCACCGACTTGTGATGG 797
 620 AGCAGTTCATCATACCAATGCTTAAGTTGGTTCACGCTCTCACCGACTTGTGATGG 561
 798 AAGGATACAAATTTGGTCCAGGATATAAATGTTGTGCACAGTTTTCAGTGCCTCCCAATTA 857
 560 AAGGATACAAATTTGGTCCAGGATATAAATGTTGTGCACAGTTTTCAGTGCCTCCCAATTA 501
 858 GTTACCGCTGTGGGAACATGCGCGCATTAATGAGATAGATGAACAATGAATCGGTCTT 917
 500 GTTACCGCTGTGGGAACATGCGCGCATTAATGAGATAGATGAACAATGAATCGGTCTT 441
 918 TTCTTCAGTTCGAAACAGACCGCGGCAAGTGAACCCAGATGTGACGCGGAAGACTCCCTG 977
 440 TTCTTCAGTTCGAAACAGACCGCGGCAAGTGAACCCAGATGTGACGCGGAAGACTCCCTG 381
 978 ATTACTTTCTGTAACATGCGCTATACATGTTACCTTTTACTTACTGAATGTTCTGTAT 1037
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 1038 AGTCACCTTCCATGAAGCAGTTTGCCTCGAATGAAGATACCTCCCTCATGATCTAGTAG 1097
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 1278 ATCGATCAGAGACTTCTATGGAAGAGTAGCAGATGTTGGAACAAACGTTTCACTCCACAC 1337
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 1338 CTACTGTATATGGCATGCTC 1357
 20 CTACTGTATATGGCATGCTC 1

RESULT 3
 BJ591074/c
 LOCUS
 DEFINITION BJ591074 normalized full length cDNA library, chloronemata, caulonemata and malformed buds Physcomitrella patens subsp. patens cDNA clone pphb42k24 3', mRNA sequence.
 ACCESSION BJ591074.1 GI:37833062
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT

Query Match 54.0%; Score 736.8; DB 3; Length 75
 Best Local Similarity 99.1%; Pred. No. 9.1e-207;
 Matches 741; Conservative 0; Mismatches 7; Indels

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 QY 678 GTTGTGGATGGGCAATTTACACAGAGTGCGGTTTACTTTTGGTCA 737
 DB 692 GTTGTGGATGGGCAATTTACACAGAGTGCGGTTTACTTTTGGTCA 633
 QY 738 AGCAGTTCATCATACCAATGCTTAAGTTGGTTCACGCTCTCACCG 797
 DB 632 AGCAGTTCATCATACCAATGCTTAAGTTGGTTCACGCTCTCACCG 573
 QY 798 AAGGATACAAATTTGGTCCAGGATATAAATGTTGTGCACAGTTTTCAGTGC 857
 DB 572 AAGGATACAAATTTGGTCCAGGATATAAATGTTGTGCACAGTTTTCAGTGC 513
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 DB 512 GTTACCGCTGTGGGAACATGCGCGCATTAATGAGATAGATGAACAAT 453
 QY 918 TTCTTCAGTTCGAAACAGACCGCGGCAAGTGAACCCAGATGTGACGCG 977
 DB 452 TTCTTCAGTTCGAAACAGACCGCGGCAAGTGAACCCAGATGTGACGCG 393
 QY 978 ATTACTTTCTGTAACATGCGCTATACATGTTTACTTACTGAAT 1037
 DB 392 ATTACTTTCTGTAACATGCGCTATACATGTTTACTTACTGAAT 333
 QY 1038 AGTCACCTTCCATGAAGCAGTTTGCCTCGAATGAAGATACCTCCCTCA 1097
 DB 332 AGTCACCTTCCATGAAGCAGTTTGCCTCGAATGAAGATACCTCCCTCA 273
 QY 1098 TATGAAGTTATCTCTTTGAAGTGTGTTGTTCCCTTTTGTAGTACTGCTC 1157
 DB 272 TATGAAGTTATCTCTTTGAAGTGTGTTGTTCCCTTTTGTAGTACTGCTC 213

Email: tshini@genes.nig.ac.jp
 A backbone of the vector is basically from pBluescri that was in vivo excised from a l-FIC phage vector (2001). 5' end of the cDNA that was digested with Xho I to SalI site of the vector and the 3' end including ligated to BamHI site of the vector (5'-gagAGAGAGATCCACCCCTGGAGAGTTTTTTTTTTT used as a 1st 3' primer, and 5'-ggTCTCGATCTGCTGTTCCAGACAGCGATGACTCGAGAACGNN 5'-hairpin primer, giving the following 5' boarder AGCCAAATCGGCGAGCTCGAATTCGCGAGACCG). cDNA insert amplified with conventional T7 and T3 primers. This cDNA library was generated according to the method of Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then the BCDATG medium for 13-14 days under the continuc These clones are available from RIKEN Bio Resource (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). of Physcomitrella EST clones is available at the PH (http://moss.nibb.ac.jp).
 Location/Qualifiers
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 /clone="pphb42k24"
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 chloronemata, caulonemata and malformed bud

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DB 212 TCATAAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTAACTGCCGCAAGAGGAGCA 153
QY 1218 GTGTCAAATGGTTGCAAGGTTATAGTGATTAGGGAAGAAAGTAGACATGTTACTTCAA 1277
DB 152 GTGTCAAATGGTTGCAAGGTTATAGTGATTAGGGAAGAAAGTAGACATGTTACTTCAA 93
QY 1278 ATCGATCAGACACTTCTATGGAAGAAAGATGACGATGGTGGAAACACACGTTCTATCTCCAC 1337
DB 92 ATCGATCAGACACTTCTATGGAAGAAAGATGACGATGGTGGAAACACACGTTCTATCTCCAC 33
QY 1338 CTACTGTATATGGCATGCTCGAGCTGC 1365
DB 32 CTACTGTATATGGCATGCTCTTGAGAGC 5

RESULT 4
BJ976562/c
LOCUS BJ976562 762 bp mRNA linear EST 14-JUN-2005
DEFINITION BJ976562 ppsep full-length cDNA library Physcomitrella patens subsp.
ACCESSION BJ976562
VERSION BJ976562.1 GI:67726303
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
1 (bases 1 to 762)
Nishiyama,T., Fujita,T., Sakakibara,K., Shin-i,T., Kohara,Y. and
Hasebe,M.
Physcomitrella patens EST from young sporophytes with surrounding
archegonia
JOURNAL Unpublished (2005)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsbini@gene.nig.ac.jp
Mosses were grown for 1-1.5 months at 25C under continuous light
followed for 3-4 weeks at 15C under short-day conditions (8L16D).
Tiny sporophytes with surrounding archegonia were dissected under
stereomicroscope and their RNA was extracted for constructing a
full-length cDNA library. The database of the EST clones is
available at the PHYSCObase (http://moss.nibb.ac.jp).

FEATURES
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Matches 758; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 634 CGAGGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATGATCGTTGTGGATGGGGCAT 693
DB 702 CGAGGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATGATCGTTGTGGATGGGGTAT 643

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QY 694 TTCACACGAGGTGCCGGTTATATCTTTTGGTCAAGATATTTCAGAGCAGT 753
DB 642 TTCACACGAGGTGCCGGTTATATCTTTTGGTCAAGATATTTCAGAGCAGT 583
QY 754 CAATGGTCTAAGTTTGGTTCGACGTGCTCACCGCTGTGTGATGGAAGAT. 813
DB 582 CAATGGTCTAAGTTTGGTTCGACGTGCTCACCGCTGTGTGATGGAAGAT. 523
QY 814 CCAGGATAAAAATCTGTGCACAGTTTTTCAGTGCCTCCCAATTTACTGTTACC 873
DB 522 CCAGGAT-AAAATGTTGTGCACAGTTTTTCAGTGCCTCCCAATTTACTGTTACC 464
QY 874 CATGGCCGCCATAATGGAGATAGATAAACAATGAATCGGTCCTTTCTTC. 933
DB 463 CATGGCCGCCATAATGGAGATAGATAAACAATGAATCGGTCCTTTCTTC. 404
QY 934 AGCACCCGGCAAGTGAACCCAGATGTGACGCGAAGACTCCTGATTACT 993
DB 403 AGCACCCGGCAAGTGAACCCAGATGTGACGCGAAGACTCCTGATTACT 344
QY 994 ATGCGCTATACATCGGTACCTTTTACTTACTGAAATGTTTCTGTATAGTCAC 1053
DB 343 ATGCGCTATACATCGGTACCTTTTACTTACTGAAATGTTTCTGTATAGTCAC 284
QY 1054 AGCAGTTTGGCCCTGAATGAAGATGACTCCCTCATGATCTAGTAGTATGAA 1113
DB 283 AGCAGTTTGGCCCTGAATGAAGATGACTCCCTCATGATCTAGTAGTATGAA 224
QY 1114 TTGAAGTGTGTTGTTCCCTTTTATAGTACTGCTCCTCTGTTCAATTCATAA 1173
DB 223 TTGAAGTGTGTTGTTCCCTTTTATAGTACTGCTCCTCTGTTCAATTCATAA 164
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DB 163 AGAACAACTGAGATGTTGTGAATGTAATCTGACGCAAGAGGAGCAGTGTC 104
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QY 1294 TATGGAAGAGATGA-CGATGTTGGAACAAACGTTTCATCTCCAC 1335
DB 43 TATGGAAGAGATGATCGATGTTGGAACAAACGTTTCATCTCCAC 1

RESULT 5
BJ585338/c
LOCUS BJ585338 706 bp mRNA linear
DEFINITION BJ585338 normalized full length cDNA library, chloro-
caulonemata and malformed buds Physcomitrella patens
ACCESSION BJ585338
VERSION BJ585338.1 GI:37827326
KEYWORDS EST.
SOURCE Physcomitrella patens subsp. patens
ORGANISM Physcomitrella patens subsp. patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Phys.
1 (bases 1 to 706)
Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide
Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y.,
Kohara,Y. and Hasebe,M.
Comparative genomics of Physcomitrella patens gametophyte
transcriptome and Arabidopsis thaliana: implication
evolution
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
JOURNAL 12808149
PUBMED Contact: Tadasu Shin-i
COMMENT Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856

```


Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp
A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XhoI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGGATCCACACCTGGAGAGTGTTCCTTTTNN-3' was used as a 1st 3' primer, and 5'-gggtctcgatcgctgttccagacagcgatcgagacggnnn-3' as 2nd 5' hairpin primer, giving the following 5' boarder sequence, AGCCAAATGCGCCGAGCTCAATCTCGAGAACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCObase (<http://moss.nibb.ac.jp/>).

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
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/tissue_type="mixture of chloronemata and malformed buds"
/clone_lib="normalized full length cDNA library, chloronemata, caulonemata and malformed buds"

ORIGIN

Query Match 51.1%; Score 697.8; DB 3; Length 706;
Best Local Similarity 99.6%; Pred. No. 3.4e-195;
Matches 699; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB |
DB 706 ATTCAGAGTGGCCGACGAGGCGCGATGTGTACTTCTGTCTGTGATCCAGATGAT 647
QY 677 CGTTGTGATGGGCAATTCACCGAGTGCCGGTTATATCTTTTGGTCAAGATATTGCA 736
DB |
DB 646 CGTTGTGATGGGTAATTCACCGAGTGCCGGTTATATCTTTTGGTCAAGATATTGCA 587
QY 737 GAGCAGTTCAATCATACCAATGCTTAAGTTGGTGTGACAGTGCTCAACAGCTGTGATG 796
DB |
DB 586 GAGCAGTTCAATCATACCAATGCTTAAGTTGGTGTGACAGTGCTCAACAGCTGTGATG 527
QY 797 GAAGGATACAAATTTGTGCGCAGGATAAAATGTTGTACAGTCTTCAGTGCCCGCAATTAC 856
DB |
DB 526 GAAGGATACAAATTTGTGCGCAGGATAAAATGTTGTACAGTCTTCAGTGCCCGCAATTAC 467
QY 857 TGTTACCGCTGTGGGAACATGCGCCCAATAATGGAGATAGATGAACCAATGCGTCT 916
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DB 466 TGTTACCGCTGTGGGAACATGCGCCCAATAATGGAGATAGATGAACCAATGCGTCT 407
QY 917 TTTCTTCTGAGTGAACACGACGCGCGCAAGTGAACCAAGTGAACCGGGAAGACTCCT 976
DB |
DB 406 TTTCTTCTGAGTGAACACGACGCGCGCAAGTGAACCAAGTGAACCGGGAAGACTCCT 347
QY 977 GATTACTTCTGTAACATGCGCTATACATGTAACCTTTTACTTACTCAATTTCTGTA 1036
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DB 346 GATTACTTCTGTAACATGCGCTATACATGTAACCTTTTACTTACTCAATTTCTGTA 287
QY 1037 TAGTCACCTTCCATGGAAGAGTGTGGCCCTGAATGAAGATACCTCCCTCATGATCTAGTA 1096
DB |
DB 286 TAGTCACCTTCCATGGAAGAGTGTGGCCCTGAATGAAGATACCTCCCTCATGATCTAGTA 227
QY 1097 GTATGAAGTATCTCTTTGAAGTGTGTGGCCCTTTTGAAGTGTGTGGCCCTTTTGAAGTGTGT 1156
DB |
DB 226 GTATGAAGTATCTCTTTGAAGTGTGTGGCCCTTTTGAAGTGTGTGGCCCTTTTGAAGTGTGT 167

QY 1157 TTCATAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTAATCGCGT 1216
DB |
DB 166 TTCATAAGTTGCCTTCAGAACAACTGAGATGTTGTGAATGTAATCGCGT 107
QY 1217 AGTGTCAATGTTGCAAGGGTTATAGTGATTTAGGAGAAAGAGGTAGCACF 1276
DB |
DB 106 AGTGTCAATGTTGCAAGGGTTATAGTGATTTAGGAGAAAGAGGTAGCACF 47
QY 1277 AATGATCAGAGACTTCTATGAAAGATGACGATGGTGGAA 1318
DB |
DB 46 AATGATCAGAGACTTCTATGAAAGATGACGATGGTGGAA 5

RESULT 6

BJ599008/c

LOCUS

DEFINITION

706 bp mRNA linear

BJ599008 normalized full length cDNA library, chloro

caulonemata and rhizoid-like protonemata Physcomitre

subsp. patens cDNA clone pphn25005 3', mRNA sequence

BJ599008

BJ599008.1 GI:37841000

EST.

Physcomitrella patens subsp. patens

Physcomitrella patens subsp. patens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Bryophyta; Funariidae; Funariales; Funariaceae; Phys

1 (Bases 1 to 706)

Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide

Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y.,

Kohara, Y. and Hasebe, M.

Comparative genomics of Physcomitrella patens gametoc

transcriptome and Arabidopsis thaliana: implication

evolution

Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2

12808149

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescri

that was in vivo excised from a 1-FLC phage vector (

2001). 5' end of the cDNA that was digested with Xho

to SalI site of the vector and the 3' end including

ligated to BamHI site of the

vector (5'-GAGAGAGAGGATCCACACCTGGAGAGTGTTCCTTTT

used as a 1st 3' primer, and

5'-gggtctcgatcgctgttccagacagcgatcgagacggnnn

5' hairpin primer, giving the following 5' boarder s

AGCCAAATGCGCCGAGCTCAATCTCGAGAACCG). cDNA insert

amplified with conventional T7 and T3 primers. This

cDNA library was generated according to the method c

Nishiyama et al. (2003).

Protonemata were blended by the POLYTRON, and then c

the BCDATG medium for 13-14 days under the continu

These clones are available from RIKEN Bio Resource C

(<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>).

of Physcomitrella EST clones is available at the PH

(<http://moss.nibb.ac.jp/>).

Location/Qualifiers

1..706

/organism="Physcomitrella patens subsp. pat

/mol_type="mRNA"

/sub_species="patens"

/db_xref="taxon:145481"

/clone="pphn25005"

/tissue_type="mixture of chloronemata, caul

rhizoid-like protonemata"

/clone_lib="normalized full length cDNA lib

chloronemata, caulonemata and rhizoid-like

transcriptome and Arabidopsis thaliana: implication evolution	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)	12808149	COMMENT	Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp A backbone of the vector is basically from pBluescript that was in vivo excised from a l-PUC phage vector (2001). 5' end of the cDNA that was digested with XhoI to SalI site of the vector and the 3' end including the ligated to BamHI site of the vector(5'- gagAgagAggATCCAAACCTCGgAggATTTTTTTTTTTT used as a 1st 3' primer, and 5'-gggtCTcGagTCATcGtGTTCcAGcAGcGatGACTcGAgAACCGNNN 5'-hairpin primer, giving the following 5' boarder s AGGCCAAATCGCGGAGCTCGAAATGTCGAGAACCG) cDNA insrt amplified with conventional F7 and T3 primers. This cDNA library was generated according to the method d Nishiyama et al. (2003). the BCDATG medium for 13- 14 days under the continuo These clones are available from RIKEN Bio Resource C (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). of Physcomitrella EST clones is available at the PHY. (http://moss.nibb.ac.jp).
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		/tissue_type="mixture of chloronemata, caul.	rhizoid-like protonemata"		
		/clone_lib="normalized full length cDNA lib	chloronemata, caulonemata and rhizoid-like:		
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	Best Local Similarity	99.2%;	Pred. No. 6.5e-182;		
	Matches	656;	Conservative	0;	Mismatches 5;
	Indels	0;			
QY	705	GTCCGGTTATACATTTTGGTCAAGATATTGCAGAGCAGTTCATCATATACC.			A 764
DB	666	GTCCGGTTATACATTTTGGTCAAGATATTGCAGAGCAGTTCATCATATACC.			A 607
QY	765	GTTCGGTTGCACGTGCTCACACAGCTTGTGATGGAAGGATACAATTTGGTGC.			A 824
DB	606	GTTCGGTTGCACGTGCTCACACAGCTTGTGATGGAAGGATACAATTTGGTGC.			A 547
QY	825	ATGTTGTTCACAGTTTTCAGTGCCTCCCAATTTACTGTTCACCGCTGTGGGAC.			A 884
DB	546	ATGTTGTTCACAGTTTTCAGTGCCTCCCAATTTACTGTTCACCGCTGTGGGAC.			A 487
QY	885	TAATGGAGATAGATGAACCAATGAATCGGTCTTTCTTTCAGTTTCGAACCA.			C 944
DB	486	TAATGGAGATAGATGAACCAATGAATCGGTCTTTCTTTCAGTTTCGAACCA.			C 427
QY	945	AAAGTGAACCAAGATGTGACCGCGGAAGACTCTCTGATTTACTTTCTGTAAACA.			C 1004
DB	426	AAAGTGAACCAAGATGTGACCGCGGAAGACTCTCTGATTTACTTTCTGTAAACA.			C 367
QY	1005	ATGTTACTCTTTTACTTACTGATTTGTTCTGATAGTACCTTCCATGGAA.			C 1064
DB	366	ATGTTACTCTTTTACTTACTGATTTGTTCTGATAGTACCTTCCATGGAA.			C 307
QY	1065	CCTGAATGAAGATACTCCCTCATCATCTAGTATGAGTATGAGTTATCTTTCTT			T 1124

Db 306 CCTGAATGAAGTACTCCCTCATGATCTAGTAGTGAAGTATCTTCTTTGAAGTGT 247

Qy 1125 GTTCCCTTTTGTAGTACTGCTCTCTGTTCAATTCATAAGTTGCTTCAGAACAACTGA 1184

Db 246 GTTCCCTTTTGTAGTACTGCTCTCTGTTCAATTCATAAGTTGCTTCAGAACAACTGA 187

Qy 1185 GATGTTGTAATGTAACTGCGACAAGAGGAGCAGTGTCAATGGTTGCAAGGGTTATAGTG 1244

Db 186 GATGTTGTAATGTAACTGCGACAAGAGGAGCAGTGTCAATGGTTGCAAGGGTTATAGTG 127

Qy 1245 ATTAGGAAAGAGGTAGCAGATGTTACTTCAATCGATCAGAGACTTCTATGGAAGA 1304

Db 126 ATTAGGAAAGAGGTAGCAGATGTTACTTCAATCGATCAGAGACTTCTATGGAAGA 67

Qy 1305 TGACGATGTTGGAACAAAGTTTCATCTCCACACTACTGTATATGCGATGCTCGAGCTCG 1364

Db 66 TGACGATGTTGGAACAAAGTTTCATCTCCACACTACTGTATATGCGATGCTCTTGAGAG 7

Qy 1365 C 1365

Db 6 C 6

RESULT 8

AY104802

LOCUS Zea mays PC069597 mRNA linear HTC 18-FEB-2005

DEFINITION Zea mays PC069597 mRNA sequence.

ACCESSION AY104802

VERSION AY104802.1 GI:21207880

KEYWORDS HTC.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 1429)

AUTHORS Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, P., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H. Jr.

TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization

JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)

REFERENCE 2 (bases 1 to 1429)

AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

JOURNAL Unpublished (2002)

REFERENCE 3 (bases 1 to 1429)

AUTHORS Coe, E.H.

TITLE Direct Submission

JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

Location/Qualifiers

1..1429

/organism="Zea mays"

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/db_xref="MaizeGDB:633782"

/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public

contigs to seed Dupont contigs; this resource assembled by Dupont as part of a collaborative overgo addressing of BACs in conjunction with Mapping Project"

ORIGIN

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Best Local Similarity 75.7%; Pred. No. 5.2e-159;
Matches 727; Conservative 0; Mismatches 233; Indels 1;

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Db 210 GGTTTGAGGGGAGAGCGCAGAGCAAGCGCGCAGCAGATGCCATCGCAGC C 269

Qy 95 CGGCAGATAGAGCAGCTCTCGAGGTGCAAGCGGTTGTGCGAGTTGAGGT A 154

Db 270 CGCCAGATCTCGAGCTCGGGATTGCAAGTTCTGCTGAGGCGGAGGT A 329

Qy 155 TGTGATCAAGCTCGGACGATCTTGGTGGAGGAGTGGAAACGT-GCAGCCCC C 213

Db 330 TGGCAGCAGGCCAAGCGCATCTCATGAGGAGTGGAAACGTGGCAGCCCC C 389

Qy 214 TGTACGGTTTCCGCTGACATCCATGGCCGAGTTTCATGATCTCATCGAGC T 273

Db 390 CGTCACTGTCTGCGCGCAGCATCCACGGCCAGTTCTACGACCTCATCGAGC T 449

Qy 274 AGGAGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGGACTATGTGC A 333

Db 450 CGGTGGCGACGGCCCGACACCACTACTCTTTATGGGCGACTACGTCC A 509

Qy 334 TTATTTCTGTGAGACTGTGTGCTCTTAGTGGCCCTGAAAGGTGCGGTATP T 393

Db 510 CTACTCAGTCAGACTGTGTCTTATTGGTGGCTCTAAAGTAGCTTATP T 569

Qy 394 CACATCTTGGCGGGAAACACGAGAGCAGCAGATTAACGCAAGTATATC A 453

Db 570 CACAATATTGAGAGGAAATCATGAGAGTAGACAAATAACTCAAGTGTATC A 629

Qy 454 TGAATGCTCGGGAAGTATGAAATGCGAAATGTTTGGAAAGTACTTTCACGC A 513

Db 630 TGAATGCTCGGGAATATGAAATGCGAAATGTTGGAAGTACTTTCACGC A 689

Qy 514 CTACCTGCTCTGACAGCTCTCATTTGAGCAGAGATTTTGTCTTTCATC C 573

Db 690 TTATTTGCTCTCACAGCTCTTATAGAAATCAGATCTTCTGCTTACATC C 749

Qy 574 TCCATGCTCGACACATPAGATCATCCGAGCCCTAGATCGTATTCACG A 633

Db 750 TCCATCACTGGATACTTTGGATAATGTCCGCTCCCTTGATCGCATACAAG A 809

Qy 634 CGAGGCGCGATGTGATCTACTCTGCTGTGATCCAGATGATCGTTGTC T 693

Db 810 TGAAGGACCTATGTGTATCTTTTGTGCTGACCCGGATGACAGATGTC T 869

Qy 694 TTACACCGAGGTCCGGTTATATCTTTTGGTCAAGATATTGCGAGCAGT C 753

Db 870 TTACACCGAGGTGCTGGATACATTTGGCAGATATTGCAACAAAT C 929

Qy 754 CAATGGTCTAAGTTTGGTTGCACTGTCTCACAGCTTGTGATGGAAGGA T 813

Db 930 AAATGGGCTAAGTCTTATTTCAAGAGCTCATCAACTTGTAAATGGAAGGT G 989

Qy 814 CCAGGTAATAATCTGTTCAGATTTTCAGTGGCCCAATTAATCTGTTTAC A 873

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Qy 874 CATGCCCGCCATAAATGGAGATAGATAAACAATGAATCGGTCTTTTCTTC C 933

Db 1050 CATGCTGGATCTCGAAATTTGGCGAGAACATGATCAGAACTTCTTCC C 1109

Qy 934 AGCACCGCGGCAAGTGAACAGATGTGACCGGGAAGACTCCTGATTAAT C 993

Db 1110 AGCTCCGCGGAGATTGAGCCGGACATGACGCGCAAGACCCAGACTACT C 1169

he
ize

Schachter V., Weissenbach J., Schlanoubat M.
URGV INRA, Clermont C. Caboché M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
[http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
length)
<http://www.genoscope.cns.fr/cgi-bin/qzb/qzb?source=Arabidopsis>.

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Dd	226 TAAACCGTTATCGAGGCGGATGTGAGGACGCTTTTGGCATCAAGCGAGAGCGATCCTTGT 285
Qy	181 GGAGGAGTGAACCGTGCAGCCGCTGAAGTGTCCCTGTCAACGCTTTTGGCGTGACATCCATGG 240
Dd	286 CGAGGAATAAATGTTTCAGCCGGTGAAGTGTCCCTGTGTAACGCTTTGCGCGATTTACGG 345
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Dd	346 CCAGTTTATGACCTTATTGAGCTCTTTCGTATCGGTGGCAAACGCTCTGTACTAACTA 405
Qy	301 CTGTGTTTCATGGCGGACTATGTGGATCTGGATATATTCTGTTCGAGACTGTGCGCTCTT 360
Dd	406 CCTCTTCATCGGAGACTATGTAGATCGTGGCTACTATTTCAGTAGAGACAGTTTCTCTATT 465
Qy	361 AGTGGCCCTCAAGGTGCGGTATAGGGATAGGATCACAAATCTTGGCGGGAAACACAGAG 420
Dd	466 GTTGGCACTAAAGTGGCGATACAGGGATAGACTTACAATCTTACGAGGGAATCACAGAG 525
Qy	421 CAGGCAGATTACCGAAGTATATGTTTTCTATGATGAATGCTCGCGGAAGTATGGAATGC 480
Dd	526 TCGGCAGATTACTCAAGTCTATGTTTTTATGACGAATGCTTGGAGGAATACGGAATGC 585
Qy	481 GAATGTTTGAAGTACTTTCACGGATCTGTTGCACTACCTGCTCTGAACGCTCTCATGTA 540
Dd	586 TAACGCTCTGGAAGTATTTTACAGACCTTTTCGATTATCTTCTTACCGCCCTCATAGA 645
Qy	541 GCACGAGATTTTGTCTTCTCATGSGTGTCTGTCTCCATCGCTGCACATTAGATACAT 600
Dd	646 GAGTCAGTTTTCTGTTTGAATGAGGGCTTTTCACTTTCTCTGGATACTCTTGTATAATAT 705
Qy	601 CCGAGCCCTAGATCGTATTCAAGAAGTGCOCGACGAGGGCCCCGATGTGTGATCTPATCTG 660
Dd	706 CCGNAGCTTGGATCGGATACNGGAGGTTCCACACGAGGACCTATGTGTGNTTATTATG 765
Qy	661 GTCTGATCCAGATGATCGTTGTGGATGGGCAATTTCCACAGAGGTGCCGGTTATACTTT 720
Dd	766 GTCTGATCCTGATGATCGATGATGAGTGGGAATATCTCCACGAGGTGCTGGTTATACATT 825
Qy	721 TGGTCAAGATATTTCGAGAGCGATTCAATCATACCAATGGTCTAAGTTTGGTTGCAAGTGC 780
Dd	826 TGGAAGGATATCGCAGCTCAATTTAATCAACAATTCGACTAAGTCTCATATCAAGAGC 885

Qy	781	TCACGAGCTGTGATGGAAGGATACAAATTCGTGTCAGGATAAAATATGTC	
Db	886	GCATCAACTTGTTCATGGAAGGTTTAACTGCTGTGTCAGGATAAGAATGTGC	
Qy	841	CAGTGGCCCCAAATTTACTGTTTACCGCTGTGGGAACATGGCCGCCATAATGG	
Db	946	TAGTGACCAAACTATTTGCTACCGGTGTGGAACATGGCTGCCATTTCTAG	
Qy	901	AACAATGAATCGGTCTTTTCTTCAGTTTCGAAACAGCACCCGCGGAAAGTC	
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Qy	961	GAGCGGAGACCTCGATTACTTTCGTAA 991	
Db	1066	TATCGGAAGACCCCTGATTATTTTTGTGA 1096	
RESULT 11			
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LOCUS			
DEFINITION			
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KEYWORDS			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
gene			
ORIGIN			

Matches	706;	Conservative	0;	Mismatches	225;	Indels	0;	Gaps	0;
Qy	61	GGTTGGCAAAATGCCGTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTGCGAGTG	120						
Db	166	GCTTTTCAAGATGCCGTGCGAACCGAGATCTGGACCGTCAGATCGAGCAGCTGATGGAGTG	225						
Qy	121	CAAGCCGTTGTCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGTT	180						
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Qy	181	GGAGGAGTGGAAACGTCAGCCGCGTGAAGTGTCTGTGCACGCTTTGCGGTGACATCCATGG	240						
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Qy	301	CTTGTTTCATGGGCGACTATGTGGATCGTGGATTAATTTCTGTGAGACTGTGTGCTCTTT	360						
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Qy	481	GAATGTTTGGAACTACTTCAGGATCTGTTTCGACTACTCTGCTCTGACGCTCTCATTTGA	540						
Db	586	TAAACGTCGGAAGTATTTTACAGACCTTTTTCGATTATCTTCTCTTACCCTCCATAGA	645						
Qy	541	GCACGAGATTTTGTCTCATGTTGCTGTCTCTCCATCGCTCGACACATTTAGATCACAT	600						
Db	646	GAGTCAGTTTTCTGTTTGCATGAGGGCTTTTACCTTCTCTGGATACTCTTGATTAATAT	705						
Qy	601	CCGAGCCCTAGATCGTATTCAAGAAGTGCCTGACGAGGGCCGATGTGTATCTACTCTG	660						
Db	706	CCGAAGCTTGGATCGGATACAGGAGGTTCCACACGAAGGACCTATGTGTGATTTATTATG	765						
Qy	661	GTCTGATCCAGATGATCGTTGTGATCGGGCATTTTACCACGAGGTGCCGGTTATATCTTT	720						
Db	766	GTCTGATCTCTGATGTCGATGTGGATGGGGAATATCTCCAGAGGTCTCGTTTATACATT	825						
Qy	721	TGGTCAAGATATTGCAGACGAGTTTCAATCATACCAATGGTCTAAGTTTGGTTGCACGTGC	780						
Db	826	TGGACAGGATATCGCAGCTCAATTAATCAACAAATGGATAAGTCTCATATCAAGAGC	885						
Qy	781	TCACCAAGCTTGTGATGGAAGGATACAATTTGGTGCAGGATAAAATTTGTTCACAGTTTT	840						
Db	886	GCATCAACTTGTCTGGAAGGTTTTAACTGCTGTGAGGATAAGAATGTGCTGACTGTGTT	945						
Qy	841	CAGTGGCCCAATTTACTTTTACCGCTGTGGGACATGGCCGCATATGAGGATAGATGA	900						
Db	946	TAGTGCACCAAACTATTGTCTACCGGTGTGAAACATGGCTGCCAATCTAGAGATAGAGA	1005						
Qy	901	AACAATGAATCCGCTCTTTTCTTCAGTTTCGAACACGACACCGCGGCAAAAGTGAACCAAGAT	960						
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RESULT 12
CNSOADNP
LOCUS
CNSOADNP 1278 bp mRNA linear HTC 06-FEB-2004
DEFINITION
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTFB16ZA06 of Flowers and buds of strain col-0 of Arabidopsis
thaliana (thale cress).

ACCESSION	BX813410
VERSION	BX813410.1
KEYWORDS	HTC; GSLT cDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e rosid; eurosid II; Brassicales; Brassicaceae; Arab 1 (bases 1 to 1278)
AUTHORS	Castell, V., Aury, J.M., Jaillon, O., Wincker, P., Clep Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Scha Temple, G., Caboche, M., Weissenbach, J., and Salanoubat Whole Genome Sequence Comparisons and 'Full-length' A Combined Approach to Evaluate and Improve Arabidop Annotation
TITLE	
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1278)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@ge - Web : www.genoscope.cns.fr]
COMMENT	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotat V., Aury J.M., Jaillon O., Wincker P., Menard M., Cr Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the genome released by MIPS (Munich Information center f Sequences). 5 prime and 3 prime are assembled with p http://www.genoscope.cns.fr/externe/sequences/Banque length
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Matches	702; Conservative 0; Mismatches 229; Indels 0;
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Qy	121 CAAGCCGTTCTCGAGTGTGGAGTGGAAGACCTATTGTGATCAAGCTCGGA
Dd	227 TAAACCGTTATTCGAGGGCGGATGTGAGGACGCTTTGCGATCAAGCGGAGAG
Qy	181 GGAGGAGTGAACGCTGCAGCCCGTGAAGTGCTCTGTCCACGGTTTCGGGTG
Dd	287 CGAGGATATATGTTTCAGCCGGTGAAGTGCTCTGTTACCGTTTGGCGCG
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Qy	301 CTGTGTCATGGGCGACTATGTGATCGTGATATTATTCTGTGAGACTGT
Dd	407 CCTCTTCATGGGAGACTATGTAGATCGTGCTACTATTTCAGTAGAGACAG
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ACCESSION AY108657
VERSION AY108657.1 GI:21211829
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1534)
Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villeda,H.,
Fang,Z., Morgante,M., Landewe,T., Fengler,K., Useche,F.,
Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.
Jr.
Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
overgo hybridization
Plant Physiol. 134 (4), 1317-1326 (2004)
15020742
2 (bases 1 to 1534)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
3 (bases 1 to 1534)

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AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, Unive
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physi
these are publicly available from ZmDB and may be fc
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When tl
maize cDNA sequences is either Virginia Walbot, Star
Schnable, Iowa State, then clones may be requested f
www.zmdb.iastate.edu.
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assembled by DuPont as part of a collaborat
overgo addressing of BACs in conjunction wi
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1 (bases 1 to 1250)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J., and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
Unpublished
2 (bases 1 to 1250)
Genoscope.
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life technologies (a division of invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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REFERENCE 1 (bases 1 to 849)
AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
TITLE     Global assembly of Cotton ESTs
JOURNAL   Unpublished (2004)
COMMENT   Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 1303057 seqs, 888780828 residues

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Listing first 45 summaries

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SUMMARIES

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4	512.4	37.5	1541	3	US-09-949-016-590
5	510.2	37.4	1843	3	US-09-780-045-10
6	505.2	37.0	2181	3	US-09-780-049-17
7	505.2	37.0	2182	3	US-09-949-016-5543
8	505.2	37.0	2966	3	US-09-780-049-3
9	501.2	36.7	1787	3	US-09-300-958A-39
10	493.2	36.1	1781	3	US-09-780-049-10
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17	389.8	28.6	1360	3	US-09-825-497A-41
18	344.8	25.3	614	3	US-09-533-559-46
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ALIGNMENTS

RESULT 1

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; Sequence 8, Application US/09828302
; Patent No. 6818805

; GENERAL INFORMATION:

; APPLICANT: COSTA E SILVA, OSWALDO DA

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: CHEN, ROUYING

; APPLICANT: ISHITANI, MANABU

; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N

; FILE REFERENCE: 16313-0029

; CURRENT APPLICATION NUMBER: US/09/828,302

; CURRENT FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/196,001

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

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QY	121	CAACCGTTGTCGGAGTTGGAGGTGAGAACTATGTATCAAGTCGGA	GT 180	
Db	121	CAACCGTTGTCGGAGTTGGAGGTGAGAACTATGTATCAAGTCGGA	GT 180	
QY	181	GGAGGAGTGGAACTGCGAGCCCGTGAAGTCTCTGTCTACGGTTTGGCGTG	GG 240	
Db	181	GGAGGAGTGGAACTGCGAGCCCGTGAAGTCTCTGTCTACGGTTTGGCGTG	GG 240	
QY	241	CCAGTTTCATGATCTCATCGAGCTTTCCGATAGGAGGCAAGCGCCCG	TA 300	
Db	241	CCAGTTTCATGATCTCATCGAGCTTTCCGATAGGAGGCAAGCGCCCG	TA 300	

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QY 301 CTTGTTCAATGGCGCACTATGTGGATCGTGGATATTATTCTGTGCGAGACTGTGTGCTCTTT 360
Db |||||
QY 301 CTTGTTCAATGGCGCACTATGTGGATCGTGGATATTATTCTGTGCGAGACTGTGTGCTCTTT 360
Db |||||
QY 361 AGTGCCCTGAAGGTGCGGTATAGGATAGGATCAATCTTGCAGGGAACACGAGAG 420
Db |||||
QY 361 AGTGCCCTGAAGGTGCGGTATAGGATAGGATCAATCTTGCAGGGAACACGAGAG 420
Db |||||
QY 421 CAGGCAGATTACCGCAAGTATATGGTTTCTATGATGAATGCCCTGCGGAAGTATGGAATGTC 480
Db |||||
QY 421 CAGGCAGATTACCGCAAGTATATGGTTTCTATGATGAATGCCCTGCGGAAGTATGGAATGTC 480
Db |||||
QY 481 GAATGTTGGAAAGTACTTCACCGATCTGTTCGACTACCTGCTCTGACAGCTCTCATTTGA 540
Db |||||
QY 481 GAATGTTGGAAAGTACTTCACCGATCTGTTCGACTACCTGCTCTGACAGCTCTCATTTGA 540
Db |||||
QY 541 GCACGAGATTTTTCTTCATGTTGTTCTGCTCCATCGCTCGACACATTAGATCACAT 600
Db |||||
QY 541 GCACGAGATTTTTCTTCATGTTGTTCTGCTCCATCGCTCGACACATTAGATCACAT 600
Db |||||
QY 601 CCGAGCCCTAGATCGTATTCAAGAAGTGC CGCAGGAGCCCGATGTGTGATCTACTCTG 660
Db |||||
QY 601 CCGAGCCCTAGATCGTATTCAAGAAGTGC CGCAGGAGCCCGATGTGTGATCTACTCTG 660
Db |||||
QY 661 GTCTGATCCAGATGATCGTTGTTGGATGGGCAATTTCA CCAAGAGTGC CGGTTATACTTT 720
Db |||||
QY 661 GTCTGATCCAGATGATCGTTGTTGGATGGGCAATTTCA CCAAGAGTGC CGGTTATACTTT 720
Db |||||
QY 721 TGGTCAAGATATTCAGAGCAGTTCAATCATACCAATGGTCTAAGTTGGTGGACGTGC 780
Db |||||
QY 721 TGGTCAAGATATTCAGAGCAGTTCAATCATACCAATGGTCTAAGTTGGTGGACGTGC 780
Db |||||
QY 781 TCACAGCTTGTGATGGAAAGATACAATTTGGTCCAGGATAAAATGTTGTCAACAGTTTT 840
Db |||||
QY 781 TCACAGCTTGTGATGGAAAGATACAATTTGGTCCAGGATAAAATGTTGTCAACAGTTTT 840
Db |||||
QY 841 CAGTGC CCCC AATTA CTGTTACCGCTGTGGGAACATATGCGCCCATTAATGGAGATAGTGA 900
Db |||||
QY 841 CAGTGC CCCC AATTA CTGTTACCGCTGTGGGAACATATGCGCCCATTAATGGAGATAGTGA 900
Db |||||
QY 901 AACATGAATCGGCTCTTTCTTCAGTTCCGAACCGACACCGCGGCAAGTGAACCAAGATGT 960
Db |||||
QY 901 AACATGAATCGGCTCTTTCTTCAGTTCCGAACCGACACCGCGGCAAGTGAACCAAGATGT 960
Db |||||
QY 961 GACGCGGAAGACTCCTGATTA CTGTTGTAACATGGCCCTATACATGGTACCTTTTACTT 1020
Db |||||
QY 961 GACGCGGAAGACTCCTGATTA CTGTTGTAACATGGCCCTATACATGGTACCTTTTACTT 1020
Db |||||
QY 1021 ACTGAATTGTTCTGTATAGTCACTTCCATGGAAGCAGTTTGCCCTGTAATGAAGATACT 1080
Db |||||
QY 1021 ACTGAATTGTTCTGTATAGTCACTTCCATGGAAGCAGTTTGCCCTGTAATGAAGATACT 1080
Db |||||
QY 1081 CCCTCATGATCTAGTAGTGAAGTTATCTTTTGAAGTGTGTTCCCTTTTACTGTA 1140
Db |||||
QY 1081 CCCTCATGATCTAGTAGTGAAGTTATCTTTTGAAGTGTGTTCCCTTTTACTGTA 1140
Db |||||
QY 1141 CTTGCTCTCTGTTCAATTCATAAAGTTGCTTTCAGAACTGAGATGTTGTGAATGTAA 1200
Db |||||
QY 1141 CTTGCTCTCTGTTCAATTCATAAAGTTGCTTTCAGAACTGAGATGTTGTGAATGTAA 1200
Db |||||
QY 1201 CTGCGACAAGAGAGCAGTGTCAATGGTTGCAAGGTTATAGTGAATTAGGGAAGAAGGT 1260
Db |||||
QY 1201 CTGCGACAAGAGAGCAGTGTCAATGGTTGCAAGGTTATAGTGAATTAGGGAAGAAGGT 1260
Db |||||
QY 1261 AGCAGATGTTACTTCAAAATCGATCAGAGACTTCTATGGAAGATCAGATCGTGGAAAC 1320
Db |||||
QY 1261 AGCAGATGTTACTTCAAAATCGATCAGAGACTTCTATGGAAGATCAGATCGTGGAAAC 1320
Db |||||
QY 1321 AACGTTCACTCCACACCTACTGTATATGGCATGTCTCGAGCTCGC 1365
Db |||||
QY 1321 AACGTTCACTCCACACCTACTGTATATGGCATGTCTCGAGCTCGC 1365
Db |||||
```

```
RESULT 2
US-09-780-045-3
; Sequence 3, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATA
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0130
; CURRENT APPLICATION NUMBER: US/09/780,045
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 3
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (991)...(1920)
US-09-780-045-3
```

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Query Match 37,8%; Score 515.6; DB 3; Length 25
Best Local Similarity 69.7%; Pred. No. 1.2e-160;
Matches 698; Conservative 0; Mismatches 304; Indels
```

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QY 14 GAGAGAGAGCGGATCGGTTAGGGTTTGGTGCCAGGGGGGAGGCGAGAGGT 73
Db |||||
QY 943 GCGGCGCCGGCTGGGCTCGGGATCCGGATCGGGATCGGGCCGCCAT 1002
Db |||||
QY 74 CCGTCATATGAGATGTAGACCGGAGATAGAGAGAGCTGTGCGAGTGCAG 133
Db |||||
QY 1003 CCGTTCACCAAGGAGCTGGACAGTGGGTCCAGAGCTGCAACGAGTGTAA 1062
Db |||||
QY 134 GAGTGGAGGTGAAGAACCTATGTATCAAGCTCGACAGATCTTGGTGGN 193
Db |||||
QY 1063 GAGAACCAAGTGCAGACCGCTGTGCGAGAAAGCAAGGAAATTTTAAACAA 1122
QY 194 GTGACGCCCGTGAAGTGTCTGTCA CGGTTTGGTTCGCTGACATCCATGGCCA 253
Db |||||
QY 1123 GTGACAGAGGTTCGTTGCCCTGTACTGTCTGTGGAGATGTCATGGTCA 1182
QY 254 CTCAATCGAGCTTTTCCGCATAGGAGGCAAGCGGCCGACAGAACTACTT 313
Db |||||
QY 1183 CTTATGGAACTCTTTAGAAATGGTGGAAATCACCGGATACAAACTACTT 1242
QY 314 GACTATGTGGATCGTGGATATATTCTGTGAGAGCTGTGCTCTTAGT 373
Db |||||
QY 1243 GACTATGTAGACAGAGGATATTTTCA GTGGAGACTGTGACTCTTCTTGT 1302
QY 374 GTGCGGTATAGGGATAGGATCACAATCTTGCAGGGAAACACGAGAGCAG 433
Db |||||
QY 1303 GTGCGTTATCCAGAACGCAATTAACAATTTGAGAGGAATCACGAAAGCG 1362
QY 434 CAAGTATATGGTTTCTATGATGAATGCTCGGGAAGTATGGAATGCGAA 493
Db |||||
QY 1363 CAAGTATATGGCTTTTATGATGAATGTCTGCGAAAGTATGGGAATGCCAA 1422
QY 494 TACTTTCAGGATCTGTTCCGACTACCTGCTCTGACAGCTCTCATTTGAGCA 553
Db |||||
QY 1423 TATTTTACAGATCTCTTTGATTAATCTTCCACTTACAGCTTTTAGTAGATGG 1482
QY 554 TGTCTTCAATGGTGGTCTGTCTCCATCGCTCGACACATTTAGATCACATCCG 613
Db |||||
QY 1483 TGCCTCCATGTGGGCTCTCTCCATCCATAGACACACTGGATCATATAAG 1542
QY 614 CGTATTCAGAGTGC CGCAGAGGGCCGATGTGTGATCTACTCTGCTC 673
Db |||||
QY 1543 CGTTTACAGGAAGTTCCACATGAGGGCCCAATGTGTGATCTGTATTGCTC 1602
QY 674 GATCGTTGTGATGGGCAATTTCCACAGAGGTGCGGTTTACTTTTGG 733
Db |||||
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Db 1603 GATCGTGGTGGATGGGTATTTTCCACACGCTGCTGGCTACACATTTGGGACACAGCAT 1662
Qy 734 CGAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTGGACGCTGCACACAGCTTGTG 793
Db 1663 TCTGAACCTTTACATGCCAATGGTCTCACTGGTTTCTCGTGGCCACACAGCTTGTGA 1722
Qy 794 ATGGAAGGATACAATTTGGTGGCAGGATAAAATGTTGTACAGTTTTCAGTGCCTCCCAAT 853
Db 1723 ATGGAAGGATACAATTTGGTGGTGTATGATCGGAATGGTTACCATTTTCAGTGCCTCCCAAT 1782
Qy 854 TACTGTTACCGCTGTGGAGACATGCCGCCATAAATGGAGATAGATAAACAATGATCGG 913
Db 1783 TACTGTTATCGTTGTGGGAACAGGCTGCTATCATGGAAATTAGATGACACTTTAAATAT 1842
Qy 914 TCTTTTCTTCAGTTCGAAACACACACCGCGCAAGTGAACACAGATGTGACGCGGAAGACT 973
Db 1843 TCTTTCTTCATTTGACCCAGCGCTGTGTGTGTGAGCCCTCATGTTACACGGCGCAC 1902
Qy 974 CTGATTACTTTCTGTAAACATGGCCTATACATGTTACTTT 1015
Db 1903 CCAGACTACTTCTATAAATTTCTCTGGGAAACCTGCCTTT 1944

RESULT 3
US-09-949-016-5464
; Sequence 5464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5464
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5464

Query Match 37.7%; Score 514; DB 3; Length 1522;
Best Local Similarity 72.0%; Pred. No. 2.9e-160;
Matches 670; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

Qy 86 GATGTAGACCGGCAGATGAGCAGCTGTGCGAGTGCAAGCCGTTGTGCGAGTTGGAGTGTG 145
Db 32 GAGCTGGACCACTGGGTGAGCAGCTGAACGAGTGTAAAGCAGCTGAACGAGAACCAAGTG 91
Qy 146 AAGAACCTATGTGATCAAGCTCGGACGATCTTGTGGAGGAGTGGAAGTGGAGCCGCTG 205
Db 92 CGGACGCTGTGCGAGAGGCAAGGAAATTTTAAACAAAGAAATCAAAATGTGCAAGAGTT 151
Qy 206 AAGTGTCTGTGTCACGTTTTCGGTGACATGCCATGCGCAGTTTTCATGATCTCATCGAGTT 265
Db 152 CGTTGCCCTGTACTGTCTGTGAGATGTGATGTGCAATTTTCATGATCTCATGATGATCTC 211
Qy 266 TTCCGATAGAGGAGGAGCGCCGACACGAACTACTTGTTCATGGGCGACTATGTGAT 325
Db 212 TTTAGAAATTTGGTGAATAATCACCGGATACAAACTACTTATTTCATGGTGACTATGTAGAC 271
Qy 326 CGTGGATATATTCTGTGAGACTGTGCTCTTAGTGGCCCTCAAGTGGCGGTATAGG 385
Db 272 AGAGGATATATTCTAGTGAGACTGTGACTCTTCTTGTAGCATTAAGGTGGGTATCCA 331
Qy 386 GATAGGATCACAATCTTGGAGGGAACACGAGAGCAGGACGATTTACGCAAGTATGCT 445
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Db 332 GAACGCTTACATATTTGAGAGGAATTCACGAAGCCGACAAATTTACCCG 391
Qy 446 TTCTATGATGAATGCTGCGGAAGTATGGAATGGAATGGAATGTTTGGAAATG 505
Db 392 TTTTATGATGAATGCTGCGGAAGTATGGAATGGAATGGAATGTTTGGAAATG 451
Qy 506 CTGTTCCACTACCTGCTCTGACAGCTCTCAATGAGCAGCAGAGATTTTTC 565
Db 452 CTCITTTGATTTATCTCCACTTTACAGCTTTAGTAGTGGACAGATATTCTG 511
Qy 566 GGTCTGTCTCATGCTCGACACATTTAGATCACAATCGAGCCCTAGATCC 625
Db 512 GGCCTCTCTCCATCCATAGACACACTGGATCATATAAGAGCCCTGGATCC 571
Qy 626 GTGCGGACAGAGGCGCCGATGTGTGATCTACTCTGCTGCTGATCCAGATGA 685
Db 572 GTTCACATGAGGCGCCCAATGTGTGATCTGTATGTCAGATCCAGATGA 631
Qy 686 TGGGCGATTTTCAACACAGAGTGCCTGTTTATCTTTTGGTCAAGATATTGC 745
Db 632 TGGGCGATTTTCAACACAGTGTGCTGGCTACACATTTGGACAAAGACATTT 691
Qy 746 AATCATACCAATGTCTAAAGTTTGGTTGCGACGCTGTCTACACAGCTTTGCM 805
Db 692 AACCATGCCAATGGTCTCACACTGGTTTCTGCTGCCACACAGCTTTGTAAT 751
Qy 806 AATTGGTCCAGGATAAAATGTTGTACACAGTTTTTCACTGCCCCCAATT 865
Db 752 AATTGGTGTATGATCGGAATGTGTTACCAATTTTCACTGCCCCCAATT 811
Qy 866 TGTGGAAACATGGCGCCCATTAATGGAGATAGATGAACAAATGAATCGGTC 925
Db 812 TGTGGAAACAGGCTGCTATCATGGAATTAGATGACACTTTTAAATATTC 871
Qy 926 TTCGAAACAGCAGCCGCGGCAAGTGAACCAAGATGTGACGCGGAGACTCC 985
Db 872 TTTGACCCAGCGCTCGTGTGAGCCTCATGTTACACGCGGACACCC 931
Qy 986 CTGTAAACATGGCCTATACATGTTACTTT 1015
Db 932 CTATAAATTTCTCTGGGAAACCTGCCTTT 961

RESULT 4
US-09-949-016-590
; Sequence 590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-590

Query Match 37.5%; Score 512.4; DB 3; Length 15
Best Local Similarity 71.9%; Pred. No. 1e-159;
Matches 669; Conservative 0; Mismatches 261; Indels 0;
```


QY 926 TTGAAACGACCGCGCAAGTGAACAGATGTGACGCGAAGACTCCTGTACTTT 985
|||
Db 1174 TTGACCGACGACCTGCTGTGGAGAGCCTCATGTGACCGGCGACCCGACACTACTTC 1233
|||
QY 986 CTGTAAA 992
|||
Db 1234 CTATAAA 1240
|||

RESULT 6

US-09-780-049-17
; Sequence 17, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 17
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1139)
US-09-780-049-17

Query Match 37.0%; Score 505.2; DB 3; Length 2181;
Best Local Similarity 69.1%; Pred. No. 3.2e-157;
Matches 690; Conservative 0; Mismatches 308; Indels 0; Gaps 0;

QY 10 GCGCGGAGGAGCGGATCGTTAGGGTTTGGTCCAGGGGGGAGGCGAGAGTTGGAC 69
|||
Db 158 GCGCGGCGCGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 217
|||
QY 70 ATGCGGTATATGAGATGTAGACCGGCGAGATAGAGCGAGTGTGCGAGTGAACGGTT 129
|||
Db 218 GAAGGTGTTTACCAGGAGCTGGACCGAGTGGATCGAGCAGCTGAACGAGTGAACGAGCT 277
|||
QY 130 GTGCGAGTTGGAGGTGAAGAACTATGTATCAAGCTCGAGCGATCTTGGTGGAGAGTG 189
|||
Db 278 GTCCAGTCCGAGGTCAAGAGCTCTGCGAAGAGGCTAAGAAATCTTGACAAAAGATC 337
|||
QY 190 GAACGTGACGCCCGTGAAGTGTCTGTCAAGTTTGGGTGACATCCATGCGCGAGTTTCA 249
|||
Db 338 CAACGTGCAAGAGTTTGGATGTCCAGTTACTGTGTGGAGATGTGCGGCAATTTCA 397
|||
QY 250 TGATCTCATGAGCTTTTCCGATAGGAGGAAAGGCGGCGGCGGCGGCGGCGGCGGCGG 309
|||
Db 398 TGATCTCATGGAAGTGTGTAGAAATGGTGGCAATCACCAGATACAAATTTACTTGTAT 457
|||
QY 310 GGGCGACTATGTGGATCGTGGATATTATCTGCGAGCTGTGCGCTTTAGTGGCCCT 369
|||
Db 458 GGGAGATTATGTGACAGAGGATATTATCTGAGTGAACAGTTACATGCTTTGAGTCT 517
|||
QY 370 GAAGGTGCGGTATAGGGATPAGGATCAATCTTGGCGAGGAAACCGAGAGCAGGACAGAT 429
|||
Db 518 TAAGGTGTTTACCGTGAACGATCACCATTCTTGGAGGATCATGAGAGCAGACAGAT 577
|||
QY 430 TACGCAAGTATATGTTTCTATGATGAATGCTGCGGAAGTATGAAATGCAATGTTTG 489
|||
Db 578 CACACAAGTTATGTTTCTATGATGAATGTTTAAAGAAATATGAAATGCAATGTTTG 637
|||
QY 490 GAAGTACTTACGAGTCTGTTGAGTACTGCTGAGCTCTGAGCTCTCATTGACAGAGAT 549
|||
Db 638 GAAATATTTTACAGATCTTTTGAATATCTTCTCTACTGCTTTGGTGGATGGGACAGT 697
|||
QY 550 TTTTGTCTTATGTTGGTGTCTGTCTCCATCGTCTGACACATTTAGATCATCCGAGCCT 609
|||

Db 698 CTTCTGTCTACATGTGTCTCTCTGCCATCTATAGATACACTGGATCATF
|||
QY 610 AGATCGTATTCAAGAGTCCGCGACGAGGCGCGGATGTGTGATCTACTCT
|||
Db 758 TGATCGCTTACAAAGAGTTCCCCATGAGGGTCCAATGTGTGACTTGTCTGT
|||
QY 670 AGATGATCGTTGTGATGGGCAATTTCCACGAGGTGCGGGTTATATCTT
|||
Db 818 AGATGACCGTGTGTGGGTATATCTCTCGAGAGCTGGTTACACT
|||
QY 730 TATTCGAGAGCTTCAATCATACCAATGGTCTAAGTTTGGTTGACGCT
|||
Db 878 TATTTCTGAGACATTTAATCATGCAATGGCTCACTGGTGTCTAGAG
|||
QY 790 TGTGATGGAAGATACAAATTTGGTCCAGGATAAAATGTTGTACAGATT
|||
Db 938 AGTGTGAGGGATATAAATCTGGTCCATGACCGGAATGTAGTAACGATT
|||
QY 850 CAATTACTGTTTACCGCTGTGGGAACATGCGCGCCATAATGGAGATAGATC
|||
Db 998 AACTATTGTTATCGTTGTGTGTAACCAAGCTGCAATCATGGAACTTGAGC
|||
QY 910 TCGGTCTTTTCTTCAGTTCGAACCAAGCAGCCGCGCAAGTGAACCCAGATC
|||
Db 1058 ATACTCTTTTTCGAGTTTGACCCAGCACCTCGTAGAGCGGAGCCACATC
|||
QY 970 GACTCCTGATTACTTTCTGTAAACATGGCCTTATACATG 1007
|||
Db 1118 TACCCAGACTTCTCTGTAATGAAATTTTAAACTTG 1155
|||

RESULT 7

US-09-949-016-5543
; Sequence 5543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5543
; LENGTH: 2182
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5543

Query Match 37.0%; Score 505.2; DB 3; Length 21
Best Local Similarity 69.1%; Pred. No. 3.2e-157;
Matches 690; Conservative 0; Mismatches 308; Indels

QY 10 GCGCGGAGGAGCGGATCGGTTAGGGTTTGTGCGCAGGGGGAGGGCAG
|||
Db 159 GCGCGGCGCGGAGAGCGCGGAGCGCGGCTCGGGCGGTGGCA
|||
QY 70 AATGCGGTATATGAGATGTAGACCGGAGATAGAGCAGCTGTGCGAGT
|||
Db 219 GAAGGTGTTTACCAGGAGCTGGACCATGATCGAGCAGCTGAACAGAT
|||
QY 130 GTGCGAGTTGAGGTGAAGAACTTATGTGATCAAGCTCGGACGATCTTGC
|||
Db 279 GTCCAGTCCAGGTCAGAGCCTCTGCGAAGGCTCTGCGAAGGCTAAAGAAATCTCTG
|||

S THEREOF

[illegible]

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RESULT 9
US-09-300-958A-39
; Sequence 39, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nu
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1787
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-39

```

Query Match 36.7%; Score 501.2; DB 3; Length 1787;

Position	Conservative	Mismatches	Indels	Gaps	0;
86	QY	GATGTAGACGGCAGATAGAGCAGCTCTCGAGTGCAAGCGCTTGTTCGAGATTGAGGTG	145		
207	Db	GAGTCGACCACTGGATCGAGCAGCTGAACGAGTGCAAGCAGCTGTTCGAGTCCAGGTC	266		
146	QY	AAGAACTTATGTGATCAAGCTCGGACGATCTTGGTGGAGGAGTGAACGTGCAAGCCCGTG	205		
267	Db	AAGAGCCTCTCGCAGAGGCTAAAGAAATCTGCACAAAGAAATCCAACGTGCAAGAGGTT	326		
206	QY	AAGTGTCTGTACGCTTTCGGGTGACATCCATGCGCCAGTTTCATGATCTCATCGAGCTT	265		
327	Db	CGATGTCGAGTTACTGTCTGTGAGATGTGCATGGGCAATTTTCATGATCTCATGGAAC	386		
266	QY	TTCCGCATAGGAGGCAAGCGCCCGCACACGAACTACTTGTTCATGGCGCACTATGTCGAT	325		
387	Db	TTTAGAATTGGTGGCAAAATCACAGATACAAATTAATTGTTATGGAGATTAATGTTGAC	446		
326	QY	CGTGGATATTAATCTGTTCGAGACTGTGTCCGCTCTTACTGGCCCTGGAAGTGCAGTATAGG	385		
447	Db	AGAGGATATATTTCAGTTGGAAACAGTTTACACTGCTTGTAGCTCTTAAGGTTTCGTTACCGT	506		
386	QY	GATAGATCACATCTTTCGAGGAGGACCAACGAGAGCAGGAGATTAACGCAAGTATATGGT	445		
507	Db	GAAACGATCACCAATCTTTCGAGGGAATCATGAGAGCAGACAGATCACACAAGTTTATGGT	566		
446	QY	TTCTATGATGAATGCTTCGGAAGTATGGAATGCGAATGTTTGGAGTACTTCAACGGAT	505		
567	Db	TTCTATGATGAATGTTTGAAGAAATATGGAATATGCAATGTTTGGAAATATTTTACAGAT	626		
506	QY	CTGTTCGACTACCTGGCTCTGACAGCTCTCAITTGAGCACGAGATTTTTTTGTCTTCATGGT	565		
627	Db	CTTTTTGACTATCTTCTCTCACTGCGCTTGGTGGATGGCGAGATCTTCTGCTACATGGT	686		
566	QY	GGTCTGTCTCCATCGCTCGACACATTAGATCAATCCGAGCCCTAGATCGTATTTCAAGAA	625		
687	Db	GGTCTCTCGCATCTTATAGATACACTGGATCATATCAGAGCACTTGATCGCTCAAGAA	746		

Qy	626	GTGCCGCAGAGGGCCCGATGTGTGATCTACTCTGGTCTGATCCAGATG	
Db	747	GTTCCTCCCATGAGGGTCCTCAATGTGTGACTGTGCTGGTCAGATCCAGATG	
Qy	686	TGGGGCATTTTCCACCACGAGGTGCCGGTTATACTTTTGGTCAAGATATTGCG	
Db	807	TGGGTTATATCTCTCTCGAGGAGCTGGTTACACTTTTGGCGAAGATATTTTC	
Qy	746	AATCATATCCAAATGGTCTTAAGTTTGGTTTGACGTGCTCACCGACTTGTGTA	
Db	867	AATCATGCCAAATGSCCTCACGTTGGTGTCTAGAGCTCACCCAGCTAGTGA	
Qy	806	AATTGGTGCCAGGATAAAATGTTGTGCACAGTTTTCTAGTGCCTCCCAATP	
Db	927	AACTGGTGCCATGACCGGAATGTTAGTAAACGATTTTTCAGTGTCTCCAACT	
Qy	866	TGTGGGAACATGGCCGCCATAAATGGAGATAGATGAAACAATGAATCGGTG	
Db	987	TGTGTTAACAGCTGCACATCATGGAACTTTGACGATCTCTAAATACTC	
Qy	926	TTCCGAACCCAGCACCGCGGGCAAGTGAACCCAGATGTGACCGCGGAAGACTCC	
Db	1047	TTTGACCCAGCACTCTGTAGGGCGAGCCCATGTTACTCGTCGTGTAACCC	
Qy	986	CTGTAAACATGGCCCTATACATG 1007	
Db	1107	CTGTAAATGAATTTTAAACTTG 1128	

```

RESULT 10
US-09-780-049-10
; Sequence 10, Application US/097800049
; Patent NO. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATORS
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/7800049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 10
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)...(1125)
US-09-780-049-10

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Query Match 36.1%; Score 493.2; DB 3; Length 17
Best Local Similarity 70.9%; Pred. No. 2.8e-153;
Matches 654; Conservative 0; Mismatches 268; Indels

Qy	86	GATGTAGACGGCAGATAGACAGACGTGTGCGAGTGCAGACCGTGTTCGG#	TC 145
Db	220	GAGCTGGACAGTGGATCAGCAGCTGAACGAGTGCAGACGCTCTCCG#	TC 279
Qy	146	AAGAACCTTAGTGAATCAAGCTCGGACGATCTTTGGTGGAGGAGTGGAAACGT	TC 205
Db	280	AAGAGCCCCCTGCAGAAAGGCTAAAGAAATCCTGACAAAAGAATCCAAACGT	TT 339
Qy	206	AAGTGTCTGTCAACGGTTTTGCCGTGACATCCATGGCCAGTCTTCATGATCT	TT 265
Db	340	CGATGTCCAAGTCACTGTGTGTGGAGTGTACATGGCAATTTTCATGATCT	TC 399
Qy	266	TTCCCGATAGAGGCAAGCGGCCCGCACGAACTACTTGTTCATGGGCG#	AT 325
Db	400	TTTAGAAATTGGTGTAAATGCACGAGATACAAATTAACCTGTTTATGGGAG#	AC 459
Qy	326	CGTGATATATTCTGTGTCCAGACTGTGTGCCTCTTGTAGTGGCCCTCGAAGCT	CG 385

TALYTIC SJBUNIT A

Db 460 AGAGATATTACTCTGTTGAACAGTTACACTGCTTGTAGCTCTTAAGGTTGGTTACCGA 519
Qy 386 GATAGATACAAATCTTCGAGGGAAACACGAGACGAGGATTAACCAAGTATATGGT 445
Db 520 GAGCGCATCACCATACTCCGAGGAATCACGAGACGACAGATCACACAGGTTTATGGG 579
Qy 446 TTCTATGATGATGCTCGGAGGATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 505
Db 580 TTCTACGAGGATGTTTAAAGGAATACGGAATGCAATGTTTGAATATCTTTCACAG 639
Qy 506 CTGTTTCGACTACTCCCTCTGACAGCTCTCATTTGAGCACGAGATTTTGTCTTCATGGT 565
Db 640 CTTTGTGACTATCTCTCTCACTGCTTGGTGGATGGCAGATCTTCTGTCTACAGGT 699
Qy 566 GGTCTGTCTCCATGCTCGACACATTAAGATACATCCGAGCCCTAGATGCTATTCAAGAA 625
Db 700 GGTCTGTCCATCATAGACACACTGGATCACATCCGAGCACTCGATCGCCTACAGGA 759
Qy 626 GTGCCGACGAGGGCCGATGCTGATCTACTCTGCTCTGATCCAGATGATGCTTGTGGA 685
Db 760 GTTCTCATGAGGGTCCAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 819
Qy 686 TGGGGCAATTTCAACACGAGGTCCCGTTATATCTTTTGGTCAAGATATTGACAGACAGTTC 745
Db 820 TGGGGGATATCTCTCGGGAGCTGTTATACCTTTGGCCAAAGATATTCTTGAGACATTT 879
Qy 746 AATCATCAAAATGGTCTAAGTTTGGTTGCACTGCTCCACCACTTGTGATGGAAGGATAC 805
Db 880 AATCATGCAATGGCTCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 939
Qy 806 AATTTGTCGAGGATAAATGTTGTCACAGTTTTCAGTGCCCCCAATTAAGTTTACGCG 865
Db 940 AACTGTTGCCATGACCGGAACGATGAACAAATTTTCAGTGTCTCCAACTATTGCTATCGT 999
Qy 866 TGTGGGAACATGCGGCCATTAATGAGATAGATGAACAAATGAAATCGGTCTTTCTTCAG 925
Db 1000 TGTGTTAACCAAGCTGCAATCATGGAATTTGACGACATCTTAAATATCTTCTTTCAG 1059
Qy 926 TTCGAACAGCACCGCGCAAGTGAACAGATGTCAGCGGAGACATCTCGATTAATCTTT 985
Db 1060 TTTGACCCAGCACCTCGTAGCGGAGCCACATGTCAGTCTGTCGTCGTCGTCGTCGTC 1119
Qy 986 CTGTAAACATGCGCTTATCATG 1007
Db 1120 CTGTAATGAAATGTAACCTTG 1141

RESULT 11
US-09-190-976B-11
; Sequence 11, Application US/09190976B
; Patent No. 6815187
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Horowitz, Arle
; TITLE OF INVENTION: Stimulation of angiogenesis via
; syndecan-4 cytoplasmic domain signaling pathway
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Prashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01930
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
; COMPUTER: Dell PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Microsoft Word version 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/190,976B
; FILING DATE: 12-No. 6815187-1998
; CLASSIFICATION: Unknown

; ATTORNEY/AGENT INFORMATION:
; NAME: David Prashker, Esq.
; REGISTRATION NUMBER: 29,693
; REFERENCE/DOCKET NUMBER: Bis-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (978) 525-3794
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-190-976B-11

Query Match 35.0%; Score 477.2; DB 3; Length 17;
Best Local Similarity 68.0%; Pred. No. 6e-148;
Matches 679; Conservative 0; Mismatches 318; Indels
; 1;
; 1C 69
; 1A 111
; 1T 129
; 1T 171
; 1G 189
; 1C 231
; 1A 249
; 1A 291
; 1T 309
; 1T 351
; 1T 369
; 1T 411
; 1T 429
; 1T 471
; 1G 489
; 1G 531
; 1T 549
; 1T 591
; 1T 609
; 1T 651
; 1C 669
; 1C 711
; 1A 729
; 1A 771
; 1T 789
; 1T 831
; 1C 849

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Db 832 GGTGATGGAGGATATAAAGTGGTCCATGACCCAAATGTAGTAACGATTTTCAGTGCTCC 891
Qy 850 CAATTACTGTTACCGCTGTGGGAACATGCGCCGCATATGGAGATAGATGAACAAATGAA 909
Db 892 AAACATATTGTTATCGTTGTGGTAACCAAGCTGAATCATGGAACATGATGATCTCTAAA 951
Qy 910 TCGGCTTTTCTTCAGTTTCGAACACGACCGCGGCAAAAGTGAACAGATGTGACGCGGAA 969
Db 952 ATACTCTTTCTTCAGTTTTCGACCTTGACCCAGCACC-CGCAGAGCGGAGCCACATGTTACTCGTCG 1010
Qy 970 GACTCTGATTACTTCTCTTAACATGCGCTATACATG 1007
Db 1011 TACCCAGACTACTTCTCTGTAATGAATTTTAACTTG 1048

RESULT 12
US-09-828-302-3
; Sequence 3, Application US/09828302
; Patent No. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-3

Query Match 31.3%; Score 427.6; DB 3; Length 447;
Best Local Similarity 98.9%; Pred. No. 8.7e-132;
Matches 441; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 459 GCCTCGCAAGTATGGAATGGAATGTTTGAAGTACTTTCACGATCTGTTTCGACTACC 518
Db 2 GCACAGAGAGTATGGAATGGAATGTTTGAAGTACTTTCACGATCTGTTTCGACTACC 61

Qy 519 TGCCTCTGACAGCTCTCATTTGAGCAGAGATTTTGTCTTCATGGTGGTCTGTCTCCAT 578
Db 62 TGCCTCTGACAGCTCTCATTTGAGCAGAGATTTTGTCTTCATGGTGGTCTGTCTCCAT 121

Qy 579 GCCTCGACACATTAGATCATATCCAGCGCTAGATCGTATTCAAGAAGTGGCGACGAGG 638
Db 122 GCCTCGACACATTAGATCATATCCAGCGCTAGATCGTATTCAAGAAGTGGCGACGAGG 181

Qy 639 GCCCATGTGTGATCTACTCTGTCTGATCCAGATGATGTTGTGATGGGGCATTTTCAC 698
Db 182 GCCCATGTGTGATCTACTCTGTCTGATCCAGATGATGTTGTGATGGGGCATTTTCAC 241

Qy 699 CACGAGGTCCCGGTTATATCTTTTGGTCAAGATATTGACAGAGCAGTTCATATACCAATG 758
Db 242 CACGAGGTCCCGGTTATATCTTTTGGTCAAGATATTGACAGAGCAGTTCATATACCAATG 301

Qy 759 GTCTAAGTTTGTTCACAGTGTCTACAGCTTGTGATGGAAGGATACAAATTTGGTCCGAGG 818
Db 302 GTCTAAGTTTGTTCACAGTGTCTACAGCTTGTGATGGAAGGATACAAATTTGGTCCGAGG 361

Qy 819 ATAAAAATGTTGTACAGTTTTTCACTGCCCCCAATTTACTGTTTACCGCTGTGGGAACATGG 878
Db 362 ATAAAAATGTTGTACAGTTTTTCACTGCCCCCAATTTACTGTTTACCGCTGTGGGAACATGG 921

Qy 879 CCGCCATAAT-GGAGATAGATGAAC 903
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Db 422 CGCCCATATTCGAGATAGATGAAC 447

RESULT 13
US-09-487-558B-269
; Sequence 269, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolit
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 269
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-269

Query Match 30.9%; Score 422; DB 3; Length 1134
Best Local Similarity 66.7%; Pred. No. 1.2e-129;
Matches 602; Conservative 0; Mismatches 300; Indels 3 0;

Qy 90 TAGACCGGCATAGAGCAGCTGTGCGAGTGCAGAGCCGCTTGTGCGAGTTG 149
Db 233 TTGACCAATGGAATTCAGCATTTTGAGTAATGCGAGCCACTATCAGAAGAC 292

Qy 150 ACCTATGTGATCAAGCTCGGACGATCTTTGGTGGAGGATGGAACTGCGAC 309
Db 293 GACTATGTAAATATGCGGTGGACGTTTGGAGTTCGAGAGAAATGTTAAA 352

Qy 210 GTCCTGTCAAGTTTGGGTGACATCCATGCGCAGTCTTTCATGATCTCATC 269
Db 353 TGCCTGTATACCATTTGTGTGACGTACACGGTCAATTCATGACTTGTTA 412

Qy 270 GCATAGAGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGGACTAT 329
Db 413 AGATTGTGTGCTTGTCTCTGACCAATTAACCTTTTCATGGTGATTAC 472

Qy 330 GATATTATCTGTGAGACTGTGCGCTCTTAGTGGCCCTGAAAGTGGCG 389
Db 473 GATATTATCTGTGAGACTGTGCGCTCTTAGTGGCCCTGAAAGTGGCG 532

Qy 390 GGATCACAATCTTTCGAGGGAACCAACAGAGCAGGAGATTAACGCAAGT 449
Db 533 GAATTACTATATCTTAGGGGCAATCAAGAGTCTAGGAGATTAACCAAGT 592

Qy 450 ATGATGAATGCTCGGGAAGTATGGAATGGAATGTTTGGAGTACTTTC 509
Db 593 ATGACGAATGTTTGAGAAAGTACGCGAGTGGCAACGTTGTGGAATAATGTT 652

Qy 510 TCGACTACCTGCTCTGACAGCTCTTATTGAGCAGAGATTTTGTCTT 569
Db 653 TCGATTATTTCCCGCTTACTGCGCTTGGTGGATAATAAAATCTTCTGTTG 712

Qy 570 TGTCTCCATCTCGACACATTTAGATCACAATCCGAGCCCTAGATCGTATT 629
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tion in : rni

Db	713	TCTCACCATGATAGAGACAAATAGATCAAGTTAGAGATTTAAATAGAAATACAGGAAGTGC	772
Qy	630	CGCACAGGCGCCGATGTTGATCTACTCTGGTCTGATCCAGATGATCGTTGTGGATGGG	689
Db	773	CTCAGNAGTCCNATGTGTGACCTTCTATGGTCCGATCCTGATGATAGAGGCGGATGGG	832
Qy	690	GCAATTTACCAAGAGGTGCCGGTTATCTTTTGGTCAAGATATTCAGACGACGTTCCAATC	749
Db	833	GAATCAGTCCGAGAGGTGCAGGCTTCACCTTTTGGTCAAGACATCAGTGAAGCAATTCAATC	892
Qy	750	ATACCAATGTCCTAAGTTTGGTTGTCACGCTGCACAGCTTGTGATGGAAAGGATACAAATT	809
Db	893	ACACTAATGACCTATCACTAATAGCAAGAGCTCACCAATTGGTAAATGGAAAGGATATTCTT	952
Qy	810	GGTGCCAGGATAAAATGTTGTACAGTCTTTTCAGTGCCCCCAATTACTGTTACCGCTGTG	869
Db	953	GGTCTCACAGCAAAATGTTGTCAACCAATTTTCAGTGTCTCCAAATATTGTGTATAGATGTG	1012
Qy	870	GGAAATGGCGCCCAATAAGGAGATAGATGAAACAAATGAATCGGTCTTTTCTTCAGTTCG	929
Db	1013	GTAACAGGCGGCTATTATGGAGGTGATGAAACCACTAATAGGCAATTTCTTACATACG	1072
Qy	930	AACCAAGCACCGCGCAAAGTGAACCAAGATGTGACGGGAAGACTCTCTGATTACTTCTGT	989
Db	1073	ATCATCTGTGAGACCGCGTGAACCAACCGTCCACAGGAAGACACCGGATTTATTTCTTAT	1132
Qy	990	AA 991	
Db	1133	AA 1134	

```

RESULT 14
US-09-614-221A-47
; Sequence 47, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614.221A
; PRIORITY FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 47
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-47

```

Query Match	29.6%	Score	404.4	DB	3	Length	1110
Best Local Similarity	65.5%	Pred. No.	8.7e-124				
Matches	591	Conservative	0	Mismatches	311	Indels	0
Gaps	0						
Qy	90	TAGACCGGCAGATAGACAGCTGCGAGTGCAAGCCGTTGTGCGAGTGTGGAGGTGAAGA	149				
Db	209	TTGACCAATGGATTGAGCATTTTGAGTAAATCCGAGGCCACTATCAGACAGATGTAGCAC	268				
Qy	150	ACCTATCTGATCAAGCTCGGACGATCTTGTGTGGAGGATGGAACTGCAGCCCTGGAAGT	209				
Db	269	GACTATGTAAAAATGGCGGTGACGTGTTCGAGTTTCGAGGAGATGTGTAAACCAATTAACG	328				
Qy	210	GTCCTGTTCAGGTTTGTGGTGTGACATCCATGACCAGTTTTCATGATCTCATCGAGCTTTTCC	269				
Db	329	TGCCCTGTTCACATTTGTGGTGTGACGTACACGGTCAATTCATGACTTGTGTAGACTTTTTA	388				
Qy	270	GCATAGAGGCGAAGCGCCCGACACGAACTACTTTGTTTCATGGGCGACTATGTGGATCGTG	329				
Db	389	AGATTGCTGGCCCTTGTCTTGACACCAATTAACCTTTTCATGGGTGATTACGTGATAGAG	448				

Qy	330	GATATTATTTCTGCGAGAC	CTGTGTCGCTCTTAGTGGCCCTCGAAGTCCGG'	'A 389
Db	449	GATATTATTTCTGTTGAAC	TGTATCTTTACCTAGTGTGCCATGAAAGTCAGA'	'A 508
Qy	390	GGATCACAATCTTTGCGAGG	GAACCAACGAGAGCAGGACGATTATAGCCAAGTA'	'T 449
Db	509	GAATTACGATCTGAGAGG	CAATCAAGAGTCTAGGCAGATATACCCAAGTA'	'T 568
Qy	450	ATGATGAATGCCCTGCGGA	AGATATGGAATCGGAATGTTTTCGGAAGTACTTC.	'T 509
Db	569	ATGATGAATGTTTTCAGAA	AGATACGGCAGTCCAAACGTTGCGGAAATGTTTC.	'T 628
Qy	510	TCGACTACCTGCTCTGAC	AGCTCTCATTCAGACACGAGATTTTTTGTGCTTT.	'C 569
Db	629	TCGATTAATTTTCTATAA	CCGCATTAGTAGTAATAAATTTTCTGCTG.	'C 688
Qy	570	TGTTCTCCATCCGTCGAC	ACACATTAGATCAATCGAGCCCTAGATTCGTATT.	'C 629
Db	689	TTTTCCCCCATGATAGAA	ACCATAGATCAGGTGAGAGAGTTGAAACAGAATA'	'C 748
Qy	630	CGCACGAGGCCGAGTGTG	ATCTACTCTGGTCTGATCCAGATGATCGT'	'G 689
Db	749	CTCATGAAGGTCCATATG	TGTGTGAACCTCTATGGTCAGACCCCTGACGATAGA'	'G 808
Qy	690	GCATTTTCAACACGAGST	CGCGGTATATTTTGGTCAAGATATTTGCAGAGI'	'C 749
Db	809	GAATCAGTCCCAGAGGT	GCAGGCTTCACTTTTGGACAAGATGTCAGTGAGI'	'C 868
Qy	750	ATACCAATGCTCTAAGTT	TTGGTTTGGTCAGGTCTCACACGCTTGTGATCGGA'	'T 809
Db	869	ACACTAATGATCTATCA	CTAATAAGCAAGAGCTCACCAATTTGGTAAATGGAA'	'T 928
Qy	810	GGTGCCAGGATAAAAATG	TTGTACAGTTTTCAGTGTGCCCCCAATTACTGT'	'G 869
Db	929	GGTCTCACACAGCAAAAT	TTGTGTCAACCATTTTCAGTGTCTCTAATTAATCTGC'	'G 988
Qy	870	GGAAACATGGCGCGCAT	TAATGGAGATAGATGAACAAATGAATCGGTCTTTT'	'G 929
Db	989	GTAATCAAGCAGCTATCA	TGGAAGTGGACAGAGATCATATAATAGACAATTC'	'G 1048
Qy	930	AACCAGACACCGCGCAAG	TGAACCATGTGACGCGGAAGACTCCTTGAT'	'T 989
Db	1049	ACCATCCGTAAGACAC	AGGTGAACCTAGCGTTCAGCAGAAAGACGCCAGAT'	'T 1108
Qy	990	AA 991		
Db	1109	GA 1110		

RESULT 15
US-09-487-558B-267
; Sequence 267, Application US/09487558B
; Patent NO. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558

tion in Fungi

;
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 267
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-267

Query Match 29.6%; Score 404.4; DB 3; Length 1110;
Best Local Similarity 65.5%; Pred. No. 8.7e-124; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 311;
QY 90 TAGACGGCAGATAGACGAGCTGTGGAGTGAAGCCGTTGCGAGTTGGAGGTCAAGA 149
Db |||||
QY 209 TTGACCAATGGATTGAGCAATTTGAGTAATGCGAGCCACTATCAGAAGACGATGTAGCAC 268
Db |||||
QY 150 ACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGAGTGGAACTGTGAGCCCGTGAAGT 209
Db |||||
QY 269 GACTATGTAATAATGGCGGTGGACGTGTTGTCAGTTCGAGGAGAAATGTTAAACCAATTAACG 328
Db |||||
QY 210 GTCTCTGTCAAGCTTGGCGTGACATCCATGCGCAGTTTTCATGATCTCATCGAGCTTTTCC 269
Db |||||
QY 329 TGCCCTGTTACCAATTTGTTGGTGAAGTACACGGTCAATTCATGACTTGTAGAACTTTTA 388
Db |||||
QY 270 GCATAGGAGGCAAGCGCCGACACGAACTACTTGTTCATGGCGACTATGTGATCGTG 329
Db |||||
QY 389 AGATTGGTGGCCCTTGTCTCTGACACCAATTTACCTTTTCATGGTGTATACGTGGATAGAG 448
Db |||||
QY 330 GATATATATCTGTCAGACTGTGCTCTTAGTGGCCCTGAAGTGGGGTATAGGGATA 389
Db |||||
QY 449 GATATATATCTGTTGAAACTGTATCTTACCTAGTTGCCATGAAAGTCAAGATACCCACATA 508
Db |||||
QY 390 GGATCACAACTCTGGAGGGAACACGAGAGCAGAGGAGGAGGATACGCAAGTATATGTTTCT 449
Db |||||
QY 509 GAATTCAGTACTGAGAGCAATACGAGTCTAGGAGATACCCAGTATACGGGTTTT 568
Db |||||
QY 450 ATGATGAATGCTCGGAGATGGAATGCGAATGTTTGGAACTACTTCACGGATCTGT 509
Db |||||
QY 569 ATGATGAATGTTTGAGAAAGTACGCGAGTGCACAACTGTGGAAATGTTTCACAGATCTTT 628
Db |||||
QY 510 TCGACTACCTGCTCTGACAGCTCTCATTTGACGACGAGATTTTGTCTCATGTGTGTC 569
Db |||||
QY 629 TCGATTAATTTTCTTAACCGCATTTAGTAGATAATAAAATTTTCTGTCTGCAATGGAGAC 688
Db |||||
QY 570 TGCTCTCCATCGCTCCACATTTAGATACATCCGAGCCCTAGATCGTATTTCAAGAGTGC 629
Db |||||
QY 689 TTTCCCAATGATAGAAACCATAGATACAGGTGAGAGAGTTGAACAGAAATACAGGAAGTGC 748
Db |||||
QY 630 CGCAGAGGCGCCGATGTGTGATCTACTCTGCTGATCCAGATCGTTGTGTGATGGG 689
Db |||||
QY 749 CTCATGAAGTCTTATGTGTGACCTTCTATGTCAGACCTGACGTAGAGCGGATGGG 808
Db |||||
QY 690 GCATTTCCACGAGGTGCGGTTTATCTTTTGGTCAAGATATTGCAGAGCAGTTCAATC 749
Db |||||
QY 809 GAAATCAGTCCCAGAGGTGCGGCTTCACTTTTGGACAAGATGTCACTGAGCAATTTCAATC 868
Db |||||
QY 750 ATACCAATGCTTAAGTTTGGTTGGACGTGCTCACCAGCTTTGTGATGAAGGATACAATT 809
Db |||||
QY 869 ACATTAATGATCTATCATTAATAGCAAGAGCTCACCAATGGTAATGGAAGGCTATGCTT 928
Db |||||
QY 810 GGTGCCAGGATAAAATGTTGTACAGATTTTTCAGTGCCGCCCAATTTACTGTTACCGCTGTG 869
Db |||||
QY 929 GGTCTCACCAAGCAAAATGTTGTACCAATTTTCACTGCTCTTAATTTACTGTACAGATGTG 988
Db |||||
QY 870 GGAACATGCGCCCAATATGGAGATAGATGAACAAATGAATGGGTCTTTTCTTCAGTTTCG 929
Db |||||
QY 989 GTAATCAAGCAGCTATCATGGAAGTGGAGCAGAAATCATAATAGACAATTTCTTACAGTACG 1048
Db |||||
QY 930 AACAGCAGCCGCGCAAGTGAACAGATGTGACGCGGAAGACTCTCTGATTTCTTCTGT 989
Db |||||
QY 1049 ACCCATCGTAAGACCGGTGAACCTAGCGTCAGCAGAAAGACCGCAGTACTTTTAT 1108
Db |||||

QY 990 AA 991
Db 1109 GA 1110
Search completed: December 9, 2005, 09:55:30
Job time : 283 secs

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 06:30:04, Search time 1078 Seconds
(without alignments)
10470.966 Million cell updates/sec

Title: US-10-764-259-8

Perfect score: 1365

Sequence: 1 ggcgttaacgcgcggaggag.....tatggcatgctcgagctgc 1365

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/us09_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/us09B_PUBCOMB.seq.*
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- 9: /cgn2_6/ptodata/1/pubpna/us10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/us11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1365	100.0	1365	3	US-09-828-302-8
2	1365	100.0	1365	7	US-10-764-259-8
3	596.6	43.7	1732	7	US-10-425-114-35277
4	592	43.4	1525	8	US-10-425-115-160542
5	589.6	43.2	1386	6	US-10-236-699-21
6	584	42.8	1330	6	US-10-236-699-31
7	582.8	42.7	1298	6	US-10-236-699-25
8	579.8	42.5	1195	7	US-10-437-963-40723
9	559.4	41.0	921	3	US-09-938-842A-705
10	559.4	41.0	921	3	US-09-938-842A-705
11	556.6	40.8	1879	8	US-10-425-115-149113
12	552.8	40.5	1243	7	US-10-236-699-7
13	547.6	40.1	1761	7	US-10-424-599-20866
14	531.8	39.0	924	3	US-09-938-842A-571
15	531.8	39.0	924	3	US-09-938-842A-571
16	525.8	38.5	1484	8	US-10-739-930-1189
17	517.4	37.9	1487	7	US-10-236-699-23
18	515.6	37.8	2574	7	US-10-467-008-3
19	514	37.7	1279	6	US-10-236-699-2
20	514	37.7	1531	6	US-10-210-120-42
21	514	37.7	1531	9	US-10-909-035-42
22	512.4	37.5	1529	3	US-09-880-107-2098
23	512.4	37.5	1541	9	US-10-956-157-1198

24	510.2	37.4	1580	6	US-10-388-934-575	Seq
25	510.2	37.4	1843	3	US-09-917-800A-1625	Seq
26	510.2	37.4	1843	7	US-10-191-803-84	Seq
27	510.2	37.4	1843	7	US-10-152-319A-1641	Seq
28	510.2	37.4	1843	7	US-10-467-008-10	Seq
29	507.6	37.2	1804	3	US-09-917-800A-1624	Seq
30	507.6	37.2	1804	7	US-10-191-803-83	Seq
31	507.6	37.2	1804	9	US-10-386-971-2	Seq
32	506	37.1	1738	6	US-10-388-934-574	Seq
33	505.2	37.0	2181	6	US-10-007-926A-184	Seq
34	505.2	37.0	2181	7	US-10-467-126-17	Seq
35	505.2	37.0	2181	9	US-10-936-273-20	Seq
36	505.2	37.0	2966	7	US-10-467-126-3	Seq
37	501.4	36.7	1798	8	US-10-425-115-103273	Seq
38	501.2	36.7	1787	6	US-10-291-808-39	Seq
c	499	36.6	1716	7	US-10-424-599-24013	Seq
40	498.2	36.5	1576	7	US-10-425-114-32875	Seq
41	498.2	36.5	1822	7	US-10-425-114-3464	Seq
42	498.2	36.5	2209	8	US-10-425-115-102388	Seq
43	496.2	36.4	2086	7	US-10-425-114-35289	Seq
44	493.6	36.2	1587	6	US-10-236-699-17	Seq
45	493.2	36.1	1781	7	US-10-467-126-10	Seq

ALIGNMENTS

RESULT 1
US-09-828-302-8
; Sequence 8, Application US/09828302
; Patent No. US20020152502A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-8

Query Match	100.0%	Score	1365	DB	3	Length	13
Best Local Similarity	100.0%	Pred. No.	0				
Matches	1365	Conservative	0	Mismatches	0	Indels	0
Qy	1	GGCGTTAAACCGCGGAGGAGCGGATCGGTTAGCGTTGGTTCGCGGGG					3A 60
Db	1	GGCGTTAAACCGCGGAGGAGCGGATCGGTTAGCGTTGGTTCGCGGGG					3A 60
Qy	61	GGTTGGGACAAATCCGTCATATGCAGATGTAGACCGGAGATAGAGCAGC					NG 120
Db	61	GGTTGGGACAAATCCGTCATATGCAGATGTAGACCGGAGATAGAGCAGC					NG 120
Qy	121	CAACCGGTTTCGAGTTGGAGTTGGAGTGAAGAACTATGTATCAAGTCGGA					3T 180
Db	121	CAACCGGTTTCGAGTTGGAGTTGGAGTGAAGAACTATGTATCAAGTCGGA					3T 180
Qy	181	GGAGGAGTGAACCTGCAGCCCGGAGTGTCCTGTCACCGTTTGGCGTG					3G 240
Db	181	GGAGGAGTGAACCTGCAGCCCGGAGTGTCCTGTCACCGTTTGGCGTG					3G 240
Qy	241	CCAGTTTCATCATCTCATCGAGCTTTTCCGCATAGGAGGCAAGCGCCCG					TA 300
Db	241	CCAGTTTCATCATCTCATCGAGCTTTTCCGCATAGGAGGCAAGCGCCCG					TA 300

Db 241 CCAGTTTCATGATCTCATCGAGCTTTTCGNCATAGGAGCAAGGCCCGCAGACGAACTA 300
Qy 301 CTTGTTTCATGGCGACTATGTGGATCGTGGATPATTATTCTGTCGAGACTGTGCTCTTT 360
Db 301 CTTGTTTCATGGCGACTATGTGGATCGTGGATPATTATTCTGTCGAGACTGTGCTCTTT 360
Qy 361 AGTGGCCCTGAAGTGGCGGTATAGGATAGGATCACAATCTTGCAGGAACCCAGAGAG 420
Db 361 AGTGGCCCTGAAGTGGCGGTATAGGATAGGATCACAATCTTGCAGGAACCCAGAGAG 420
Qy 421 CAGGCAGATTACGCAAGTATATGGTTTCTATGATGAATGCCCTCGCGAAAGTATGGAATGC 480
Db 421 CAGGCAGATTACGCAAGTATATGGTTTCTATGATGAATGCCCTCGCGAAAGTATGGAATGC 480
Qy 481 GAATGTTTGGAAAGTACTTCACGGATCTGTTTCGACTTACCTGCTCTGACAGCTCTCAATTGA 540
Db 481 GAATGTTTGGAAAGTACTTCACGGATCTGTTTCGACTTACCTGCTCTGACAGCTCTCAATTGA 540
Qy 541 GCACGAGATTTTTCCTCTTCATGTTGGTCTGTCTCCATCGCTCGACACATTAGATCACAT 600
Db 541 GCACGAGATTTTTCCTCTTCATGTTGGTCTGTCTCCATCGCTCGACACATTAGATCACAT 600
Qy 601 CGAGCCCTAGATCGTATTCAAGAAGTGC CGCAGAGGCCCGATGTGTGATCTACTCTG 660
Db 601 CGAGCCCTAGATCGTATTCAAGAAGTGC CGCAGAGGCCCGATGTGTGATCTACTCTG 660
Qy 661 GTCTGATCCAGATGATCGTTGGTATGGGCAATTTACACAGAGTGC CGGTTTACTTTT 720
Db 661 GTCTGATCCAGATGATCGTTGGTATGGGCAATTTACACAGAGTGC CGGTTTACTTTT 720
Qy 721 TGGTCAAGATATTCAGAGCAGTCTCAATCATACCAGTGTCTAAGTTTGGTGCACGTGC 780
Db 721 TGGTCAAGATATTCAGAGCAGTCTCAATCATACCAGTGTCTAAGTTTGGTGCACGTGC 780
Qy 781 TCACAGCTTTGATGGGAAGGATACAAATTTGGTGCAGGATAAAATGTTGTACAGATTTT 840
Db 781 TCACAGCTTTGATGGGAAGGATACAAATTTGGTGCAGGATAAAATGTTGTACAGATTTT 840
Qy 841 CAGTGC CCCCCAATTA CTGTTACCGTGTGGGAACATGCGCCGCAATAATGGAGATAGATGA 900
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Qy 901 ACAATGATCGGTCTTTCTTCAGTTCGAAACAGCA CGCGGCAAAAGTGAACAGATGT 960
Db 901 ACAATGATCGGTCTTTCTTCAGTTCGAAACAGCA CGCGGCAAAAGTGAACAGATGT 960
Qy 961 GACGCGGAAGACTCTGTACTTTCTGTAAACATGGCCTATACATGTTACCTTTTACTT 1020
Db 961 GACGCGGAAGACTCTGTACTTTCTGTAAACATGGCCTATACATGTTACCTTTTACTT 1020
Qy 1021 ACTGAATGTTCTGTATAGTCACTTCCATGGAAGCAGTTTGCCTCTGAATGAAGATACT 1080
Db 1021 ACTGAATGTTCTGTATAGTCACTTCCATGGAAGCAGTTTGCCTCTGAATGAAGATACT 1080
Qy 1081 CCCTCATGATCTAGTATGAAGTATCTCTTTGAAAGTGTCTCTCCCTTTTACTA 1140
Db 1081 CCCTCATGATCTAGTATGAAGTATCTCTTTGAAAGTGTCTCTCCCTTTTACTA 1140
Qy 1141 CTTGCTCTCTCTTCAATCATAAAGTTGCTTTCAGAACCACTGAGATGTTGTGAATGTAA 1200
Db 1141 CTTGCTCTCTCTTCAATCATAAAGTTGCTTTCAGAACCACTGAGATGTTGTGAATGTAA 1200
Qy 1201 CTGCGA CAAAGAGCAGTGTCAATGGTTGCAAGGTTTATAGTATAGGGAAGAAGGT 1260
Db 1201 CTGCGA CAAAGAGCAGTGTCAATGGTTGCAAGGTTTATAGTATAGGGAAGAAGGT 1260
Qy 1261 AGCATGTTTACTTCAATTCGATCAGAGACTTCTATGGAAAGATGACGATGGTGGAAAC 1320
Db 1261 AGCATGTTTACTTCAATTCGATCAGAGACTTCTATGGAAAGATGACGATGGTGGAAAC 1320
Qy 1321 AACGTTTCATCTCCACACCTTACTGTATATGGCATGTCTCGAGCTCGC 1365
Db 1321 AACGTTTCATCTCCACACCTTACTGTATATGGCATGTCTCGAGCTCGC 1365

RESULT 2
US-10-764-259-8
; Sequence 8, Application US/10764259
; Publication No. US20040148658A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND M
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/10764,259
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-10-764-259-8

Query Match 100.0%; Score 1365; DB 7; Length 13.
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 0; Indels 0;

Qy 1 GGCCTTAACGCGCGGAGGAGCGGATCGGTAGGTTTGGTCCAGGGG 60
Db 1 GGCCTTAACGCGCGGAGGAGCGGATCGGTAGGTTTGGTCCAGGGG 60
Qy 61 GGTGGGACAATCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 120
Db 61 GGTGGGACANTCCGTCATATGCAGATGTAGACCGGCAGATAGAGCAGC 120
Qy 121 CAAGCCGTTGTGAGGTTGGAGGTGAAGAACTATGTGATCAAGCTCGGA 180
Db 121 CAAGCCGTTGTGAGGTTGGAGGTGAAGAACTATGTGATCAAGCTCGGA 180
Qy 181 GGAGGTTGGAACCTGCAGCCCGTCAAGTGTCTGTACCGTTTGGGTG 240
Db 181 GGAGGTTGGAACCTGCAGCCCGTCAAGTGTCTGTACCGTTTGGGTG 240
Qy 241 CCAGTTTCATGATCTCATCGAGCTTTTCCGATAGGAGGCAAGGCCCGG 300
Db 241 CCAGTTTCATGATCTCATCGAGCTTTTCCGATAGGAGGCAAGGCCCGG 300
Qy 301 CTTGTTTCATGGGCGACTATGTGGATCGTGGATATTTCTGTGCGAGACTG 360
Db 301 CTTGTTTCATGGGCGACTATGTGGATCGTGGATATTTCTGTGCGAGACTG 360
Qy 361 AGTGCCCTGAAGGTCGGTATAGGATAGGATCACAATCTTTCGAGGGA 420
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Qy 421 CAGGCAGATTACGCAAGTATATGGTTTCTATGATGAATGCCCTCGCGAAGT 480
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Db 481 GAATGTTTGGAAAGTACTTCACGGATCTGTTTCGACTTACCTGCTCTGACAG 540
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Qy 601 CCGAGCCCTAGATCGTATTTCAAGAAGTGC CGCAGAGGCCCGCATGTGTG 660
Db 601 CCGAGCCCTAGATCGTATTTCAAGAAGTGC CGCAGAGGCCCGCATGTGTG 660

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1081 CCCTCATGATCTAGTATGATGAGTATCTCTTTGAAAGTGTGTTCCCTTTTACTGTA 1140
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1321 AACGTTTCATCTCCACACTTCTATATGGAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 1365
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RESULT 3
US-10-425-114-35277
; Sequence 35277, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35277
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE90H04_FLI

US-10-425-114-35277

Query Match 43.7%; Score 596.6; DB 7; Length 17
Best Local Similarity 76.9%; Pred. No. 2.9e-181;
Matches 728; Conservative 0; Mismatches 219; Indels 3 0;
QY 48 GGGGAGGCGCAGAGGTTCGGGCAATGCGCGTCATATGCAAGATGTAGACCGG 3C 107
DB 199 GGTAGAGCGGAGCGCAGCGCGATGCGCGTCGACGCGATCTGGACCAAC 3C 258
QY 108 AGCTGTCCAGTGCAGCCGTTTCGGAGTTGGAGGTGAAGAACCTATGT 1C 167
DB 259 AGCTGCGGGAATGCAAGTTCTTCCGCGAGGTGAGGTCAAGACGCTATGC 1A 318
QY 168 GGACCATCTTGGTGGAGGAGTGGAACTGTCAGCCGTCGAAGTGTCTCTGTC 3G 227
DB 319 AGGCGATCTCATGGAGGAGTGGAACTGTCAGCCGTCGCGTCCCGCTGC 3G 378
QY 228 GTGACATCCATGGCCAGTTTCATGATCTCATCGAGCTTTTCGCGCATAGGA 3C 287
DB 379 GCGACATCCACGCGCAGTTCTACGACCTCATCGAGCTCTTCGCGCATCGGC 3C 438
QY 288 CCGACACGAACCTACTTGTTCATGGCGGACTATGCGATCGTGATATTAT 3A 347
DB 439 CAGACACCAACTACTCTTTTATGGCGGATTAGTCGACCGTGGCTACTAC 3A 498
QY 348 CTGTGTCGCTCTTAGTGGCCCTGGAAGTGGCGTATAGGATAGGATCACT 1G 407
DB 499 CTGTGTCGCTTGTAGTGGCTCTTAAAGTACGTTATAGAGACAGAAATCACT 1G 558
QY 408 GGAACACGAGCAGGAGGATTAACGCAAGTATATGTTTCTATGATGAT 3A 467
DB 559 GAAATCATGAGAGCAGACAAATACTCAAGTGTATGGCTTCTATGATGAT 3A 618
QY 468 AGTATGGAATTCGNAATGTTTGGAAAGTACTTCAAGATCTGTTTCGATAC 3A 527
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QY 528 CAGCTCTCATTTGAGCAGAGATTTTGTCTTCATGTTGGTGTCTGCTCCP 2A 587
DB 679 CAGCTCTTTAGAAAACAGATCTTCTGCTTACATGGTGGTCTCTCTCP 1A 738
QY 588 CATTAGATCAGATCCGAGCCCTAGATCGTATTCAGAAAGTGCCTGCGACGAG 3T 647
DB 739 CATTGGAATAATTCGCGCCCTTGATCGCATACAAGAGGTCCACATGAT 3T 798
QY 648 GTGATCTACTCTGTTCTGATCCAGATGATGTTGTTGGATGGGCGATTTCP 1G 707
DB 799 GTGATCTTTTGTGGTCTGACCCAGATGACCGATGTTGGGTGGGGAATTTCP 1G 858
QY 708 CCGGTTATACTTTTGGTCAAGATATTCAGAGCAGTTCATCATACCAAT 1T 767
DB 859 CTGGATACAAATTTGGCCCAAGATATTCACAAACAAATTCACCATACAAAT 1C 918
QY 768 TGGTTGCAAGTGTCTCACCCAGCTTGTGATGGAAGGATACAATTTGGTGCAC 1G 827
DB 919 TTAATTCAGAGGCGACATCACTTGTATGGAAGGCTTCAATTTGGTGTCA 1G 978
QY 828 TTGTCACAGTTTTCAGTGGCCCCCAATTAATCTGTTACCGCTGTGGGAACATC 1A 887
DB 979 TTGTGACTGTGTTGAGCGCGCTAACTACTGCTACCGATGCGGAACATC 3C 1038
QY 888 TGGAGATGATGAACAAATGATGATCGTCTTTCTTCAGTTCGAAACAGCA 1A 947
DB 1039 TCGAAATTTGGGAGAACATGATCAGAACTTCTCTCAATTCGACCCAGCT 1A 1098
QY 948 GTGAACACAGATGTGACCGCGGAAGACTCTCTGATTTACTTTCTGTAAACA 95
DB 1099 TTGAGCGGACATGACCGCGCAAGACACAGACTACTTTTGTAGAAA 11

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; Sequence 160542, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 160542
; LENGTH: 1525
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1525)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_77994C.1
US-10-425-115-160542

Query Match 43.4%; Score 592; DB 8; Length 1525;
Best Local Similarity 76.0%; Pred. No. 8.3e-180;
Matches 730; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 35 GGTGTTGGTCCAGGGGGGAGGCGCAGAGTGGGACAATGGCGTCATATGCAGATGTAGAC 94
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 95 CGGCAGATAGACAGCTGTCGGAGTGCAGCGCTTGTCCGAGTTGGAGGTGAAGAACCTA 154
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 CGCCAGATCTCGACGTGGGATTCGAATTCCTGCTGAGCGGAGGTCAAACGCTA 329
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 TGTGATCAAGCTCGACGATCTTGTGTGAGGAGTGAACGTGCAGCCCGTGAAGTGTCT 214
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 330 TCGCAGCAGGCCAAGCGCATCTCATGAGGAGTGGAACTGCAGCCCGTGCCTGCCCC 389
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 215 GTCACGGTTTGGGTGACATCATCGGCAGTTTCATGATCTCATGAGCTTTTCGGCAT 274
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 GTCACTGTCTGGCGGACATCACGGCCAGTTTCTACGACCTCATCGAGCTCTTTCGCATC 449
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 275 GGAGCAAGCGCCCGACACGAACTACTTGTTCATGGCGACTATGTGGATCGTGATAT 334
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QY 450 GGTGGCGACGCGCCGACACCACTACCTCTTATGGCGACTAGTCGACCGTGGCTAT 509
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QY 335 TATTCGTGAGACTGTGTGCTCTTAGTGGCCCTGAAGGTGCGGTATAGGATAGGATC 394
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 510 TACTCAGTGGAGACTGTGTCTTATTGGTGGCTCTAAAGTACGTTATAGACAGAAATC 569
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QY 395 ACAATCTTGGAGGAAACACAGAGCAGGAGATAGCAAGTATATGTTTCTATGAT 454
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 570 ACAATATTGAGGAAATCATGAGAGTAGACAAATAACTCAAGTGTATGGTCTTATGAT 629
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 455 GAATGCCTCGGAAGTATGGAATGCGAATGTTTGGAAATGACTTCACCGGATCTGTTTCGAC 514
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 630 GAATGCTTGGGAATATGGAATGCAATGTGTGGAAGTACTTTACAGACTTGTTCAT 689
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 515 TACTGCTCTGACAGCTCTCATGAGCAGAGATTTTGTTCCTCATGTTGTTGTTCTGTCT 574
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 690 TATTTGCCCTCTCACAGCTCTTATAGAAATCAGATCTTCTGCTACATGTTGTTCTCTCT 749
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 575 CCATCGCTCGACATATAGATCACATCCGAGCCCTAGATCGTATTCAAGAGTGGCGAC 634
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 750 CCATCACTGGATACATTGGATAATGTCCGCTCCCTTGATCGCATACAAGAGTCCCGAT 809
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 635 GAGGCCCGGATGTGATCTACTCTGGTCTGATCCAGATGATCGTTGTGGATGGGCGATT 694
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 810 GAAAGACCTATGTGTGATCTTTTGTGGTCTGACCCCGATGACAGATGTGGATGGGAAAT 869
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 695 TCACCACAGGTGCGGGTTATACCTTTTGGTCAAGATATTGCGAGCAGATT 754
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 870 TCACCAAGGGGTGCTGGATACACATTTTGGCCAAAGATATTGCACCAATTT 929
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 755 AATGGTCTAAGTTTGGTTGCACGTGCTCACAGCTTCCACAGCTTGTGATGGAAGGATA 814
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 930 ANTGGCTAAGCTTATTTCAAGAGCTCATCACTTGTATGGAAGGGTT 989
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 815 CAGGATAAAATTTGTGCACAGTTTTCAGTGCCCCCAATTAAGTGTACCG 874
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 990 CAGGATAAAGAGTTGTGACAGTGTTCAGCGCGCTTAACATATTGCTACCG 1049
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 875 ATGCGCGCCATAATGGAGATAGATGAACATGAATCGTCTTTTCTTCA 934
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1050 ATGGCTCGATCTCGAAATTTGGCGAGAACATGATCAGAACTTCCTCCA 1109
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 935 GCACCGCGGCAAGTGAACCAAGATGTGACGGGAGACTCTCTGATTACTT 994
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1110 GCTCGCGGCAGATTGAGCCGACATGACGGCGCAAGACCCAGACTACTT 1169
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-10-236-699-21
; Sequence 21, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Glycine max
US-10-236-699-21

Query Match 43.2%; Score 589.6; DB 6; Length 13
Best Local Similarity 75.4%; Pred. No. 4.7e-179;
Matches 733; Conservative 0; Mismatches 239; Indels 0;

QY 20 GAGCGGATCGGTTAGGGTTTGGTGCCAGGGGGGAGGCGAGAGTTTGGGAC 79
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 41 GAATCGATCTCAGAGAAGTCCGATCTCGAGGTTGGAGCCAAACGAAAC 100
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 80 TATCGAGTGTAGACCGCAGATAGACAGCTGTGCGAGTGCAGCCGTT 139
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 101 CACCGGATCTGAGCGCAGACAGATGAGCAGCTGATGGACTGCAGCCCTCT 160
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 140 GAGGTGAAGAACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGAGTG 199
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 161 GAGGTGAAGCGCTGTGGATCAAGCGAGGACGATCTTGTGGAGAGTG 220
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 200 CCCGTGAAGTGTCTGTCAACGGTTTGGGTTGACATCCATGGCCAGTTTCA 259
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 221 CCGGTTAAGTCCCGCTCACCGTCTCGCGCGATATTACCGGCCAGTCTTA 280
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 260 GAGCTTTTCCCATAGAGGCAAGCGCCGACACAGCACTACTTGTTCAT 319
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 281 GAGCTGTTTGGATTTGGAGGAAACGCTCCCGATACCAATATCTCTTCA 340
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 320 GTGGATCGTGATATATTCTGTGAGACTGTGCTCGCTCTTAGTGGCCCT 379
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 341 GTAGATCGTGGATACTATTTCAGTGGAGACTGTTCACACTTTTGGTGGCTTT 400
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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380 TATAGGATAGGATCAAACTCTTGGAGGAAACCAGAGAGCAGGATACGCAAGTA 439
401 TATAGAGATAGATCAAACTCTTGGAGGAAATCATGAAACCGTCAAACTACTCAAGTG 460
440 TATGTTCTTATGATGAATGCTCGGAGATGAAATGCGAATGTTTGGAACTACTTC 499
461 TATGCTCTTATGATGAATGCTTGAAGAAATATGGAATGCGAATGCTTGGAAATAC 520
500 ACGGATCTGTTGAGTACCTGCTGACAGCTCTCATTTGAGCAGAGATTTTGTCTT 559
521 ACAGACTTGTGTGATATTTGCTCTGACTGCTCCCTCATTTGAGAGTCAGATTTTCTGCTG 580
560 CATGTTGTTCTGCTCTCCATGCTGCACACATTTAGATCACTCCGAGCCCTAGATCGTATT 619
581 CATGAGGTTCTCACTCTTTTGGATACACTGGATTAACATCAGAGCATTTGGATCGTATT 640
620 CAAGAAGTGGCCGACAGAGCCCGATGTTGATCTACTCTGCTCTGATCCAGATGATCGT 679
641 CAAGAGGTTCCACATGAAGAGCAATGTTGATCTCTTGTGCTCTGACCCCTGATGATGCG 700
680 TGTGATGGGATTTTCCACGAGGTCGGGTATATCTTTTGGTCAAGATATTCAGAG 739
701 TGTGATGGGATATATCTCCAGTGGTGAGGATACATTTTGGGAGGATATAGCTGCT 760
740 CAGTTCAATCATACCAATGGTCTAAAGTTTGGTTCACGCTGCTCACAGCTTGTGATGAA 799
761 CAGTTTATCATACCAATGGCTCTCCCTGATATCAGAGCACATCAGCTGTTATGAA 820
800 GGATCAATTTGTTGACAGATTAATAATGTTGTCAGTTTTTCAAGTTTTCAGTCCCAATTTACTGT 859
821 GGATTTCAATTTGTTGACAGATTAATAATGTTGTTGATCTGTTTATGTTGCTCCAAATTTACTGT 880
860 TACCGCTGTTGGAACATGCGCCATATGAGATGAGATGAACATGATCGTCTTTT 919
881 TATCATGTTGGAATATGGTCCCATATAGAGAAATAGGAGAAATATGGATCAGAAATTTT 940
920 CTTCAAGTTTCAACACGACGCGGCAAGTGAACAGATGTCAGCGGAAAGTCTCTGAT 979
941 CTTCAAGTTTCAACACGACGCGGCAAGTGAACAGATGTCAGCGGAAAGTCTCTGAT 991
980 TACTTTCTGTAA 991
1001 TATTTTGTAA 1012

RESULT 6
US-10-236-699-31
; Sequence 31, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-236-699-31

Query Match 42.8%; Score 584; DB 6; Length 1330;
Best Local Similarity 76.2%; Pred. No. 2.9e-177;

Matches 719; Conservative 0; Mismatches 225; Indels
QY 48 GGGGGAGGGCAGAGGTTGGGCAATATGCCGTATATGCAGATGTACACCGC
DB 81 GGAGGTGGGAGCGGAAACGAAACGATGCCGTCTCACGGGATCTGGAACG#
QY 108 AGCTGTCTCGAGTGCAGAGCCGTTGTTCGAGTGTGGAGTGAAGAACCTATGT
DB 141 AGCTGATGAGTGCAGAGCCTCTGTTCGAGTGGAGTGAAGCGCTGTGT
QY 168 GGAAGATCTTGGTGGAGGAGTGGAAACGTCGAGCCCGTGAAGTGTCTGT
DB 201 GGGCGATTTCTCGTGGAGGAATGGAACGTCGAAACCGGTGAAGTGGCCCGTC
QY 228 GTGACATCCATGGCCAGTTTTCATGATCTCATCGAGCTTTTCCGCATAGG#
DB 261 GCGATATTCAGCGCCAGTTTTCAGATCTCATCGAGCTGTTCGGATGGA#
QY 288 CCGACACGAATCTACTTGTTCATGGGCGACTATGTGGATCGTGGATATTAT
DB 321 CCGATACCAATATCTCTTTCATGGGTGATTATGTAGATCGTGGATATTAT
QY 348 CTGTGCTCTCTTGTAGTGGCCCTGAAAGTGGCGGTATAGGATAGGATCAG#
DB 381 CTGTTACACTTTTGGTGGCTTTTGAAGTCCGTTACAGAGATAGATCAG#
QY 408 GGAACCCAGAGCAGGAGGAGATTAACGCAAGTATATGGTTTCTATGATGAA#
DB 441 GAAATCATGAAGTCTGCAAAATTAATCAAGTGTATGGCTTCTATGATGAA#
QY 468 AGTATGGAATTCGAATGTTTGGAGTACTTTCAGCGATCTGTTTCGACTAC
DB 501 AATATGGAATTCGAATGTTTGGAGTACTTTCAGCGATCTGTTTCGACTAC
QY 528 CAGCTCTCAATTTGAGCAGAGATTTTGTCTTTCATGTTGTTGTTCTCTCT#
DB 561 CTGCCCTCAATTTGAGAGTCAAGTCTGCTTTCGCTTTCGAGAGTCTCTCACT
QY 588 CATTAGATCATATCCGAGCCCTAGATCGTATTCAGAGAGTGGCGACGAC
DB 621 CACTGGATAACATCAGAGCATTTGGATCTGTATACAGAGGTTCCCATGAP
QY 648 GTGATCTACTCTGTTCTGATCCAGATGATCTGTTGGATGGGCAATTTCT#
DB 681 GTGATCTCTTCTGTTCTGACCTCTGATGATCGTGTGGATGGGATATCT
QY 708 CCGTTATATCTTTTGGTCAAGATATTTGAGAGGATTTCAATCATACCAAT
DB 741 CAGGATACATTTTGGACAGGATATAGCTGCTCAGTTTAAATCATACCAAT
QY 768 TGGTTGACAGTCTTCCAGGCTTGTGATGGAGGATACAATTTGGTCCAC
DB 801 TGATATCGAGAGCTCATCAGCTTGTATGGAAGGATTCATTTGGTGGCAG
QY 828 TTGTTCACAGTTTTCAGTGGCCCGCAATTAATCTGTATCCGCTGTGGGAACAT#
DB 861 TGGTGTGATTTTATGTCACCAATTAATCTGTATCCGATGTGGGATATG
QY 888 TGGAGATAGATGAACCAATGAATCGGCTTTTCTTTCAGTTCGAAACGAG#
DB 921 TAGAAATAGGAGAGAAATATGATGATCAGAAATTCCTTTCAGTTTCAGCGC
QY 948 GTGAACAGATGTGACCGGAGAGTCTCTGATTTACTTTCTCTGTA 991
DB 981 TTGAGCCTGACACCAACGAGAGTCTCCAGATTTATTTTATAA 1024

RESULT 7
US-10-236-699-25
; Sequence 25, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.

; APPLICANT: CHEN, RUOYING		
; APPLICANT: ISHITANI, MANABU		
; APPLICANT: VAN THIELEN, NOCHA		
; APPLICANT: COSTA E SILVA, OSWALDO DA		
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND		
; TITLE OF INVENTION: METHODS OF USE IN PLANTS		
; FILE REFERENCE: 16313-0161		
; CURRENT APPLICATION NUMBER: US/10/236,699		
; CURRENT FILING DATE: 2002-09-05		
; PRIOR APPLICATION NUMBER: 60/317,305		
; PRIOR FILING DATE: 2001-09-05		
; NUMBER OF SEQ ID NOS: 43		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 25		
; LENGTH: 1298		
; TYPE: DNA		
; ORGANISM: Oryza sativa		
US-10-236-699-25		
Query Match	42.7%;	Score 582.8; DB 6; Length 1298;
Best Local Similarity	76.3%;	Pred. No. 7.1e-177;
Matches	716;	Conservative 0; Mismatches 222; Indels 0; Gaps 0;
Qy	54	GGG CAG AGG TTG GGA CCA ATG CCG GT CAT ATG CAG ATG TAG ACC GCG CAG ATAG CAG CAG CTGT 113
Db	159	GTG CGG GGG AGA GAG ATG CCG GT CGT CG CAC CGG GAT CTG GAC CGG CAG ATCG CG CAG CTGC 218
Qy	114	CGAG TCG AAC CGC GTT GCG AG TTG GAG GTT GGA AGA ACC TAT GTG ATC AAG CTC CGG ACG A 173
Db	219	GGG AGT TCG AAC CAC TTG CG CGG AGG GGG AG GTG AG GGG CG GTG TGC GAG CAG GCG CAA GGC CA 278
Qy	174	TC TTG GTG GAG GAG TGG AA C GTG CAG CCG CGT GAA GTG TCC TGT CAC CG TTG TCG CGT GACA 233
Db	279	TC TC TCA TGG AGA GTG GAA C GTG CAG CCG GTG CG GTG CCG CCGT CAC CG GTCTG CGG CGG ACA 338
Qy	234	TCC ATG GCC AG TTTC ATG ATCTCAT CAG ACT TTTT CCG CATAG GAG GCA AG CGCC CGC ACA 293
Db	339	TCC AGG CCA GTTCTAC GAC CCTCAT CAG ACT TTTCCG CATCG CGG CAG GCG CGCC CGC ACA 398
Qy	294	CGA CTA CT TGTTC ATG CGG CAG CTATG TGN TCG TGG ATATAT TCTGT CGA GACTGTGT 353
Db	399	CCA ACTAC CTCTTC ATG GGG CAG TAC CGT CGA CCG GTGG CTACTCTCA GTTGG AGACTGTGT 458
Qy	354	CGCTCTTAG TGG CCG CCGTGA AGTGG GTATAG GGTAG GATCA CCA ATCTTGG CAG GGA ACC 413
Db	459	CG TTG TTG GTG CTTTGA AGTAC CGCTAC AGATCG AA TTACA ATATTG AGAG GAA ATC 518
Qy	414	ACG AGC AGC AGC AGATTA CGC AAG TATATG GTTTCTATG ATG AATG CCGTGG AAGTATG 473
Db	519	ATG AGA CAG ACA AATCA CTCA AGTGTAC CGG CTTCTAC GATG AATG CTTG AAG AAAGTATG 578
Qy	474	GAA ATG CGA ATG TTTTGA AGTACTTTCA CGG ATCTG TTCG ACTACTG CTTCTG CAG AGCTC 533
Db	579	GAA ATG CAA ATGTATG GAA ATACHTTTAC AGACTTGT TTG ATATTTG CTTCTCA AGCTC 638
Qy	534	TCA TTG AGC AGC AGATTTTTTGTCTT CATGG TGGTCTGTCTCC ATTCGCTCG ACA CATTTAG 593
Db	639	TTATAG AAAAA CCA GGTG TTTCTG CCGTTCAC GGTGGTCTCTCTCC ATCATTTGG ATACTTTAG 698
Qy	594	ATC AATCCG AGCCCTAG ATCGTATTC AAG AAGTGG CCG CAG AGG GCGCCG ATGTGTG ATC 653
Db	699	ATA ACATCCG TGCTCTTG ATCGTATCA AAG AGG TTCTCTATG AAGG ACCCA ATGTGTG ATC 758
Qy	654	TACTCTG GTCTG ATCCAG ATGATCG TTGTG ATGGGG CATTTTCA CCA CAG GTG CCG GTT 713
Db	759	TTTTGTG GTCTG ACCCAG ATG CAG ATG CCG GTGGG AATTTTCA CCG CAG AGG AGC AGTT 818
Qy	714	ATACTTTTGG TCAAG ATATTG CAG AGC AGTTCA ATCATACA CCA ATGGTCTA AGTTTGG TTG 773
Db	819	ATA CATTTGGG CAA GATATCG CTC CAA CAG TTATA CCA TACA AATGGTCTATCTCTCATCT 878
Qy	774	CAG CTGCTCACC AGCTTGTGTG ATG GAA GGTATCA AATTTGG TGGCAG GATAAAA ATTTGTG CA 833

QY 493 GTACTTACGGATCTGTTGAGACTACCTGCTCTGACAGCTCTCATTTGAGCAGAGATTTT 552
DB 426 ATACTTTACAGACTGTTTGAATATTTGCTCTCAGAGCTCTTAGAAAAACAGAGTGT 485
QY 553 TTGCTCTTCATGCTGCTCTCTCCATCGCTGACACATAGATCATATCCGAGCCCTAGA 612
DB 486 CTGCTCTTCATGCTGCTCTCTCCATCATTTGATATCTTTAGATAATATCCGCTCTTTGA 545
QY 613 TCGTATTCAAGAGTCCGCGCAGAGGCGCCGATGTGTATCTCTGATCTGATCCAGAG 672
DB 546 TCGTATACAGAGGTTCTCATGAGAGGCCATGTGTGATCTTTTGTGCTGACCCAGA 605
QY 673 TGATCGTTGTGATGGGCAATTTACAGAGAGGTCGCGGTATATCTTTTGTGTTGTTCAAGATAT 732
DB 606 TGACAGATGCGGTGGGAAATTTACAGAGAGGAGCAGGTTATACATTTGGGCAAGATAT 665
QY 733 TGCAGAGAGTTCAATCATACAAATGTTCTAAGTTTGGTTGACGTGCTCACCAGCTTGT 792
DB 666 CGCTCAACAGTTTAAACCATACAAATGGTCTATCTCTCATCTCAAGGGCACAATCACTTGT 725
QY 793 GATGAAGGATACAAATGGTGCAGGATAAAAAATGTTGTCAAGATTTTCAGTGCCCCCAA 852
DB 726 AATGAAGATTTAATTTGGTGTGACGACAGAGATGTTGTGACGGTCTTCAGTGACCCAA 785
QY 853 TTACTGTTACCGCTGTGGGAACATGCGCGCCCAATAATGGAGATAGATGAACAATGAATCG 912
DB 786 CTACTGTTATCGCTGTGGTAAATGGTGAATCTCTGAGATTGGGAAACATGGATCA 845
QY 913 GTCTTTCTTCAGTTGCAACGACCGCGGCAAGTGAACAGATGTGACCGGAGAC 972
DB 846 GAATTTCTTCCAAATTTGATTCAGCTCTCTCGGCAATTTGAACAGACACAACGCAAGAC 905
QY 973 TCCTGATTACTTTCTGTAA 991
DB 906 TCCCGACTACTTTTGTAA 924

RESULT 9

US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 705
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-705

Query Match 41.0%; Score 559.4; DB 3; Length 921;
Best Local Similarity 75.5%; Pred. No. 2.1e-169;
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0;
QY 71 ATGCGCTCATATGAGATGATAGCGGAGATAGAGCTGTCGGAGTGAACGCGTTG 130
DB 1 ATGCGTTAAACGGAGATCTCGCGGTGATCGAAGACAGCTAATGGAGTGAAGCGGTTA 60

QY 131 TCGGAGTTGGAGTGGAAGAACCTATGTGATCAAGCTCGAGCATCTTGGT 390
DB 61 GGTGAAGCAGACGTCGAGATCTCTTTGCGATCAAGCTAAAGCGATCTTGT 120
QY 191 AACGTGAGCCGTCGAGTGTCTGTCACGGTTCGGGTGACATCCATGC 250
DB 121 AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATGCGGCGATATCCATGC 180
QY 251 GATCTCATCGAGCTTTTCCGCATAGGAGGCAAGGCGCCGACACCAAACTP 310
DB 181 GACCTAATTTGAGCTATTTCTGTTATGGTGGTAAATGCTCTCTGATATAATP 240
QY 311 GCGGCTATGTGGATCGTGGATATTTCTGTGAGACTGTGTGCTCTCT 370
DB 241 GAGATTTATGATAGTCGTGGCTACTATTCTGTAGAAAACAGTCTCTCTATT 300
QY 371 AAGTGGCGTATAGGATAGGATCACATCTTGGAGGGAACCCAGAGAC 430
DB 301 AAGTGGCGTTTACAGGGACAGACTTACGATCTCTGGAGGGAATCATGAGAC 360
QY 431 ACGAAGTATATGGTTTCTATGATGAATGCTCGGAAAGTATGGAATGC 490
DB 361 ACACAGTCTATGGTTTATGACGAATGCTTGAGAAATACGGAATGC 420
QY 491 AAGTACTTACCGGATCTGTCGACTACCTGCTCTGACAGCTCTCATGTF 550
DB 421 AAGTATTTTACGGACCTTTTCGATTTATCTCCTCTTACAGCACTCATAGF 480
QY 551 TTTTGTCTTCATGTTGTTCTCTCCATCGCTCGACACATTAGATCAAT 610
DB 481 TTCTGTTTGCATGAGGCGCTTTTCACCTTCTCTGGATCTCTTGACAATAT 540
QY 611 GATCGTATTTCAAGAGTGCAGGCGCCGATGTCGATGTCATCTCTC 670
DB 541 GATCGATACAGAGGTTCCACACGAGGACCAATGTCGATCTACTCTC 600
QY 671 GATGATCTTGTGATGGGCAATTTTACCAAGAGTGCCTGCTTAPACTTT 730
DB 601 GACGATCGTTGTCGATGGGAAATATCTCTCGTGGTGTGCTTACAGT 660
QY 731 ATTGACAGAGCTTCAATCATACCAATGGTCTAAGTTTGGTTGACGTC 790
DB 661 ATTGCTACTCAGTTTAAATCATAAATGAGTGTGATCTGATCTCAAGAC 720
QY 791 GTGATGGAAGGATACAAATTTGTCAGGATAAAAATGTTGTACAGTTT 850
DB 721 GTAATGGAAGCTATATTTGTCAGGAAAGAACGTTAGTACAGTGT 780
QY 851 AATTACTGTTACCCTGTGGGAACATGCGCCCATTAATGGAGATAGATG 910
DB 781 AACTACTGTTACAGATGTGGAACCATGCGCCCAATTTCTTGAGATTGGAGA 840
QY 911 CGGTCTTTTCTTCAAGTTCGAACCAAGCCGCGGCAAGTGAACCCAGATG 970
DB 841 CAGAACTTCTTCAATTCGATCCAGCACCTAGACAAGTCGAACCCGATAC 900
QY 971 ACTCTGATTAATTTCTGTAA 991
DB 901 ACCCTGATTAATTTTGTGA 921

RESULT 10

US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGE
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A									
; CURRENT FILING DATE: 2001-08-24									
; PRIOR APPLICATION NUMBER: US 60/227,866									
; PRIOR FILING DATE: 2000-08-24									
; PRIOR APPLICATION NUMBER: US 60/264,647									
; PRIOR FILING DATE: 2001-01-16									
; PRIOR APPLICATION NUMBER: US 60/300,111									
; PRIOR FILING DATE: 2001-06-22									
; NUMBER OF SEQ ID NOS: 5379									
; SEQ ID NO 705									
; LENGTH: 921									
; TYPE: DNA									
; ORGANISM: Arabidopsis thaliana									
; US-09-938-842A-705									
Query Match 41.0%; Score 559.4; DB 3; Length 921;									
Best Local Similarity 75.5%; Pred. No. 2.1e-169;									
Matches 695; Conservative 0; Mismatches 226; Indels 0; Gaps 0									
QY	71	ATGCCGCTCATATG	CAGATGTAGACCGGCAGATAGACGACGTGTCGGAGTGC	AAGCCGCTG	130				
DB	1	ATGCCGCTTAAACG	GAGATCTCGACCGTCAGATCGAACAGCTAATG	TGAGCGCTTA	60				
QY	131	TCGGAGTTGAGGTGA	AGACCTATGTGATCAAGCTCGGACGATCTTGCTGGAGAGTGG	190					
DB	61	GGTGAACGACAGCTG	GAAGATCTCTTTGGCATCAAGCTAAAGCGATCTTGTTGTTGAGGAATAT	120					
QY	191	AAGTCGAGCCCGTGA	AGTGCCTGTCACGGTTTGCCTGACATCCATGGCCAGTTTCAT	250					
DB	121	AATGTTCAACCGGTT	AAAGTGTCCGGTTACGGTATCGGCGCATATCCATGGCCAGTTTAT	180					
QY	251	GATCTCATCGAGCT	TTTTCCGCATAGGAGGCAAGGCCGCCGACACGAACTACTTGTTTCATG	310					
DB	181	GACCTAATTGAGCT	ATTTTCGTATTTGTTGTTAATGCTCTCTGATACTAATTA	240					
QY	311	GGCGACTATGTGGA	TCTGTGCGAGATGTTTCTGTGCGACTGTGTGCGCTCTTAAGTGCCCTG	370					
DB	241	GGAGATTATGTAGAT	CGTGGCTACTAATCTGTAGAAAAGTCTCTCTATTTGGTGGCAATTA	300					
QY	371	AAGTGGCGGTATAGG	GATAGATACAACTCTTGGAGGGACACGAGCAGCAGGACGAGATT	430					
DB	301	AAGTGGCGTTACAGG	ACAGACTTACGATCTCTGCGAGGGAATCATAGAGCCGTCAGATT	360					
QY	431	ACGCAAGTATATGTT	CTATGATGAATGCCCTGCGGAAAGTATGGAATTCGCAATGTTTGG	490					
DB	361	ACACAGTCTATGGT	TTTTTATGACGATGCTTTGAGGAATACGGAATGCAATGTGTGG	420					
QY	491	AAGTACTTCACGGA	TCTGTTTCGACTACTGCTCTGACGCTCTCATTTGAGCACGAGATT	550					
DB	421	AAGTATTTTACGGAC	CTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGAGTCAAGTT	480					
QY	551	TTTTTGCTTTCATGT	GGTCTGTCTCCATCGCTCGACATATTAGATCAATCCGAGCCCTTA	610					
DB	481	TTCTGTTTGATGAGG	CGCTTTCACCTTCTCTGGATATCTTTGACAACTCTTGAAGCTTTG	540					
QY	611	GATCGTATTCAGAAG	TGCCGACAGAGGCCCGGATGTGTGATCTACTCTGGTCTCATCCA	670					
DB	541	GATCGAATACNAGAG	GTTCACACGAGGACCAATGTGCGATCTACTCTGGTCTGATCCC	600					
QY	671	GATGATCGTTGTGAT	GGGCAATTTACCAAGAGTGCCGGTTATATCTTTTGGTCAAGAT	730					
DB	601	GACGATCGTTGTGAT	GGGGAATATCTCCTCGTGGTGTGGTTTACACGTTTGGACAGGAC	660					
QY	731	ATTGCAGACGATTTCA	TATCATCAACCAATGGTCTAAGTTTGGTGGACGGTCTCACCAGCTT	790					
DB	661	ATTGCTACTCAGTT	TTAATCATAAACAATGGAATGAGTCTGATCTCAAGACCGCATCAACTT	720					
QY	791	GTGATGGAAGGATACA	ATTGGTGCCAGGATAAAAATGTTGTACACAGTTTTCAGTGCCCCC	850					
DB	721	GTAATGGAAGGCTATA	TTGGTGTACGGAAGAAGACGTAGTACAGTGTGTTAGTGACCG	780					
QY	851	AATTACTGTTTACCG	CTGTGGAAACATGCCCCTATPAATGGAGATAGATGAACAATGAAT	910					

Db	781	AACTACTGTTACAGATGTGGAACATCGCCGCAATTCCTTGAGATTGGAGA	A 840
Qy	911	CGGTCTTTTCTTCAGTTTCGAACACCGCGGCAAAAGTGAAACAGATGT	G 970
Db	841	CAGAACTTCCTTCAATTCGATCCAGCACCTTAGACAAAGTCGAACCCGATAC	G 900
Qy	971	ACTCCTGATTAATCTTCTGTAA 991	
Db	901	ACCCTGATTATTTTGTGA 921	
RESULT 11			
US-10-425-115-149113			
; Sequence 149113, Application US/10425115			
; Publication No. US20040214272A1			
; GENERAL INFORMATION:			
; APPLICANT: La Roes, Thomas J.			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule:			
; TITLE OF INVENTION: Plants			
; FILE REFERENCE: 38-21(53222)/B			
; CURRENT APPLICATION NUMBER: US/10/425,115			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 369326			
; SEQ ID NO 149113			
; LENGTH: 1879			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; OTHER INFORMATION: Clone ID: MRT4577_67515C.1			
US-10-425-115-149113			
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Best Local Similarity 75.0%; Pred. No. 2.7e-168;			
Matches 722; Conservative 0; Mismatches 239; Indels 2;			
Qy	37	TTTGTGCCAGGGGGGAGGGCAGAGGTTGGGCAATGCCGTCAATGCAG.	G 96
Db	158	TTCTGCGGCGAAGGGAGCGGGCGGCGGACGAGATCGCTCGCAGGGG.	G 217
Qy	97	GCAGATAGACGAGCTGTGCGAGTCCAAAGCCGTTGTCCGAGTTGGAGGTGA	G 156
Db	218	GCAGATCGCGAGCTGCGCGACTGCCAGTACTGCCCAGGCGGAGGTCA	G 277
Qy	157	TGATCAAGCTCGGACGATCTTGTGGAGGAGTGGAACTGCGAGCCCGTGA	T 216
Db	278	CGAGCAGCCCAAGGCCATCTCTATGGAGGAGTGGAACTGCGAGCCCGTGC	T 337
Qy	217	CACGGTTTGGGTTGACATCCATGCCAGTTTCATGATCTCATCGAGCTTT	G 276
Db	338	CACCGTCTGGCGGACATCCAGGCCAGTTCTATGACCTCATCGAGCTCT	G 397
Qy	277	AGGCAAGCGCCCGACACGAACTACTTGTTCATGGCGCACTATGTGGATC	A 336
Db	398	CGGCGACTCTCCGACACCAACTACCTCTTCATGGCGACTACGTCGATC	A 457
Qy	337	TTCTGTGAGACTGTGTGCTCTCTAGTGGCCCTGAGGTGCGGTATAGGG.	C 396
Db	458	TTCAAGTTGAACACAGTTTTCTCTGTTAGTGGCTTTTGAAGTCCGTTACAGAG.	C 517
Qy	397	AATCTTCGAGGGGAAACACAGAGAGCAGGACAGATTACGCAAGTATATGGTT	A 456
Db	518	AATCTTAGAGAAATCATGAGACGACGACAAATCACTCAAGTATATGGCT	A 577
Qy	457	ATGCTTCGGAAGTATGGAAATGCGAAATGTTTGGAAAGTACTTTCACGGATC	A 516
Db	578	ATGCTTAAGAAAAATATGAAATGCAATGTCTGGAAGTATTTTACAGACT	T 637
Qy	517	CTGCTCTGACAGCTCTCATTTAGCAGCAGAGATTTTTGTCTCTCATGGTG	C 576
Db	638	TTTGCCCTCTCAGCTCTTATAGAAAATCAGGTCTCTGTCTCTCATGGTG	C 697


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; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1761)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118848C.1
US-10-424-599-20866

Query Match      40.1%; Score 547.6; DB 7; Length 1761;
Best Local Similarity 76.5%; Pred. No. 2.1e-165;
Matches 710; Conservative 0; Mismatches 214; Indels 4; Gaps 3;

QY 68 ACAATCGCGTCAATATGCAGATAGACCGGAGATAGAGCAGCTGTGGAGTGAAGCG 127
Db 306 ACGATGCCGTCTCACGCGGATCTGAGCGACAGATCGAGCAGCTGATGGACTGCAAGCCT 365

QY 128 TTGTCGGAGTTCGAGGTGAAGAACCTATGTGATCAAGCTCGACAGATCTTGGTGGAGG 187
Db 366 CTGCGGAGTCGAGGTGAAGGCGCTGTGCGATCAAGCGAGGCGGATCTTGTGGAGGAG 425

QY 188 TGGAAAGTGCAGCCCGTGAAGTGTCTGTACCGGTTTGGCGTGCACATCCATGCCCGATTT 247
Db 426 TGGAAAGTGCAGCCCGTGAAGTGTCTGTACCGGTTTGGCGTGCACATCCATGCCCGATTT 485

QY 248 CATGATCTCATCAGCTTTTCGCGATAGGAGCAAGCGCCCGACAGCACTACTTGTTC 307
Db 486 TAGCATCTCATCAGCTTTTCGCGATAGGAGCAAGCGCTCCCGATACCAATTTATCTCTTT 545

QY 308 ATGGGGGACTATGTGATCGTGATATATTCTGTGAGACTGTGT - CGCTCTTGTATGCG 366
Db 546 ATGGGGGAAATATGTAGATCGTGATATATTCTGTGAGACTGTGTACGCTTTTGTGAC 605

QY 367 CCTGAAGTGCAGGTATAGGATAGATCAAA - TCTTGGAGGGAACCAAGAGCAGGC 425
Db 606 CTTGAACGTTCTTATGATAGATAAATTAACAATCTTATGGGAAATCATGAAGCGCTC 665

QY 426 AGATTACGCAAGTATATGTTTCTATGATGAATGCTCGGGAAGTATGGAATGGAATG 485
Db 666 AATAAATCAATGATGATGCTTCTATGATGAATGCTTGGAGAAATATGGAATGCAATG 725

QY 486 TTTGGAAGTACTTACCGGATCTGTTGCGACTACTG - CCTCTGACAGCTCTCATTTAGCA 543
Db 726 TCTGGAATATCTTACAGACTTGTGATTAATTTGATCTCTGACGCTTATTTAGAG 785

QY 544 CGAGATTTTTGTCTTCAATGTTGTCTCCATCGCTCGACACATAGATACATCGG 603
Db 786 TCAGATTTTCTGTTGATGAGGTTCTTCAACATCTTTGGATACACTTGTGAATATCGG 845

QY 604 AGCCCTAGATCGTATTCAGAAAGTCCGCGACGAGGCCCGATGTGTGATCTACTCTGTC 663
Db 846 TGCCCTTGGATCGCATACAGAGGTTTCCACAGGAAGCAATGTGTGACCTCTTGTGTC 905

QY 664 TGATCCAGATGATCGTTGTTGGATGGGGCATTTTCCACAGAGTGGCGGTTTACTTTTGG 723
Db 906 TGATCCAGATGATCGTTGTTGGATGGGGCATTTTCCACAGTGTGGTGTGATACATTTGG 965

QY 724 TCAAGATATTGACAGCAGTTCAATCATACCAATGTTCTAAGTTTGGTTGTCAGTCTCA 783
Db 966 ACAGGATATAGCTGCTCAGTTTAAATCATACCAATGTTCTCCCTGATATCGAGACTCA 1025

QY 784 CCAGCTTGTGATGGAAGGATACAAATTTGTCAGGATAAATTTGTCACAGTTTTCAG 843
Db 1026 CCAGCTTGTGATGGAAGGATCAATTTGTCAGGATAAATTTGTCAGTGTGTTTGTAG 1085

QY 844 TGCCCCCAATTAATCTGTACCGTGTGGGAACATAGGCCGCCATAATGAGATAGATGAAC 903
Db 1086 TGCAACCAATTAATCTGTACCGATGTGGGAACATAGCTGCGCATCTAGAAATTTGGAGNA 1145

QY 904 AATGAATCGGCTTTTCTTCAATGTTGAAACAGCA CCGCGGCAAAAGTGAACCAAGATGTGAC 963
Db 1146 TATGATCAGAAATTTTCTGAGTTTGTATCCAGTCTCCAGACAAATTTGAGCCCGACACAC 1205
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QY 964 GCGAAGACTCTCGATTACTTTCTGTAA 991
Db 1206 ACGAAGACTCCAGATTATTTTGTAA 1233

RESULT 14
US-09-938-842A-571
; Sequence 571. Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571

Query Match      39.0%; Score 531.8; DB 3; Length 92.
Best Local Similarity 73.7%; Pred. No. 1.8e-160;
Matches 677; Conservative 0; Mismatches 242; Indels 0;

QY 73 GCCGTCAATATCAGATGTAGACCGGAGATAGAGCAGCTGTCGGAGTGCA 132
Db 6 GCCGCGACCGAGATATCGATCGTCAGATCGAGCAGCTTATGGAGTGTA 65

QY 133 GGAGTTGGAGTGAAGAACCTATGTATCAAGCTCGGACGATCTTTGGTGG 192
Db 66 TGAAACGGAGTGAAGATGTTGTGAGCAGCAGAAAGCAGTCTTGTGG 125

QY 193 CGTGAGCCCGTGAAGTGTCTGTCA CGGTTTGGGTGACATCCATGGCC 252
Db 126 TGTTCACCGGTTAAATGTCCGGTTACCGTCTGCGGTGATATCCACGGCC 185

QY 253 TCTCATCGAGCTTTTCCGATAGGAGGCAAGCGCCGACACGAACTACT 312
Db 186 TCTAATCGAGCTTTTTCGATCGGTGGTTCTTCTCGATACATAATATC 245

QY 313 CGACTATGTGATCGTGATATTATCTGTGAGACTGTGTGCGCTCTTAG 372
Db 246 TGATTTATGTATCGAGGATATTATCTGTGAGACAGTCTCACCTTTGG 305

QY 373 GGTGCGGTATAGGATAGGATACAAATCTTCCGAGGGAACCAACGAGAGCA 432
Db 306 AGTTGTTACAGAGATAGACTTACTATCTTAAGAGGAATCATGAAAGCC 365

QY 433 GCAAGTATATGTTTCTATGATGAATGCTCGGGAAGTATGGAATGCGA 492
Db 366 TCAAGTGTATGGTTTATGATGAATGTTTGGAGGAATATGGAATGCTA 425

QY 493 GTACTTCAGGATCTGTTTCGACTACCTCCCTCTGACAGCTCTCATTTGAGC 552
Db 426 GCACCTTCACTGATCTTTTGTGATTTCTTCCACTTACAGCTCTTATTGAG 485

QY 553 TTGCTTCAATGGTGTCTGTCTCCATCGCTCGACATATAGATACATCC 612
Db 486 CTGTTTACATGGAGACTTTTCACTCTTTTATAGATACACTTGAACAACATCC 545

QY 613 TCGTATTCAAGAAGTGGCCGACGAGGGCCCGATGTGTGATCTACTCTGCT 672
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Db 546 TCGAATTCAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTTATGTCTGATCCAGA 605
QY 673 TGAATCGTGTGATGGGATTTCCACAGAGGTGCGGTGTATACCTTTTGGTCAAGATAT 732
Db 606 TGACCGATCGGTGGGGAATATCTCTCGTGTGAGGCTACACTTCCGGAAGAATAT 665
QY 733 TGCAGAGCAGTTCAATCATACCAATGGTCTAAAGTTTGGTTGCAAGTGTCTCACAGCTTGT 792
Db 666 CGCTACTCAGTTTAAACCAACCAATGGACTCTCTGATTTCAAGAGACATCACTTGT 725
QY 793 GATGGAAGGATCAATGTGTGCAAGGATAAATGTGTGACAGTTTTCAGTGCCCCAA 852
Db 726 CATGGAAGGTTTAAATGGTGCCAAAGAAAGACGTTGTGACTGTATTTAGTGCCCAA 785
QY 853 TTACTGTACCGCTGTGGGAACATGCGCCCAATATGGAGATAGATGAACATGAATCG 912
Db 786 CTATTGCTACCGTGTGGCAACATGGCTGCGATTTCTAGAGATCGGTGAGAACATGSA 845
QY 913 GTCTTTTCTTCAAGTTCGAACACGACCGCGCAAGTGAACAGATGTGACCGGAAGAC 972
Db 846 GAATTTCTTCAAGTTTGTATCCAGTCCAGTCCAGTCAAGTCCGAACCGCAACCACT 905
QY 973 TCCTGATTAATTTCTGTAA 991
Db 906 TCCAGATTATTTTGTAA 924

RESULT 15
US-09-938-842A-571
; Sequence 571, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571

Query Match 39.0%; Score 531.8; DB 3; Length 924;
Best Local Similarity 73.7%; Pred.No.1.8e-160;
Matches 677; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

QY 73 GCGGTCAATATGAGATGTAGACCGGAGATAGAGCAGTGTGCGAGTGAAGCCGTTGTC 132
Db 6 GCGGCGGACCGGAGATATCGATCGTCAAGTCAAGCAGCTTATGGAGTGTAAAGCGTTATC 65
QY 133 GGAGTTGGAGGTGAAGAACCTATGTATCAAGTCCGAGCATCTTGGTGGAGAGTGA 192
Db 66 TGAACCGGAGGTGAAGATGTTGTGTGAGCAGCAGCAAGACGATTTCTTGTGAAGAGAT 125
QY 193 CGTGACGCGCGTGAAGTGTCTGTGACGTTTGGTGGTGCATCCATGCGCAGTTTCATGA 252
Db 126 TGTTCAACCGGTAAATGTCCCGTTTACCGTCTGCGGTGATATCCAGCGCAATTTTACGA 185
QY 253 TCTCATCGAGCTTTTCCGATAGGAGGCAAGCGGCCGACAGAACTACTTCTTCATGGG 312
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Db 186 TCTAATCGAGCTTTTTCGTATCGGTGGTTCTTCTCTGTATCACTAATTTATC
QY 313 CGACTATGTGATCGTGTGATATTTATTTCTGTGAGACTGTGTGCGTCTTTAC
Db 246 TGATTTATGTGATCGAGGTATTTATTTCTGTGAGACAGTCTCACCTTTTGG
QY 373 GGTGCGGTATAGGATAGGATCACAATCTTTCGAGGGAACACACGAGAGCA
Db 306 AGTTCGTTACAGAGATAGACTTACTATCTTAAGAGGGAATCATGAAGCC
QY 433 GCAAGTATATGTTTCTATGATGAATGCTTCGGAAGTATGGAATGCGF
Db 366 TCAAGTGTATGGTTTTATGATGAATGTTTGAAGAAATATGAAATGCTF
QY 493 GTACTTCAAGGATCTGTTTCGACTACCTCGCTGTGACAGCTCTCATTTGAC
Db 426 GCATTTCACTGATCTTTTGTGATTTCTTCCACTTACAGCTCTTATTGAGF
QY 553 TTGTCTTCATGGTGTCTGTCTTCCATCGTCCGACACATTAGATCACATCC
Db 486 CTGTTTATCATGGAGACTTTTCACTTCTTTAGATACACTTGACAACATCC
QY 613 TCGTATTCAGAAGTGTGCGACGAGGCGCGATGTGTGATCTACTCTGGT
Db 546 TCGAATTCAGAGGTTTCCACATGAAGGACCAATGTGTGATCTCTTATGGT
QY 673 TGATCGTTGTGATGGGCAATTTCAACACAGGTCGCGGTTATACTTTTC
Db 606 TGACCGATGCGGTTGGGAATATCTCTCGTGTGTCAGGCTACACTTTTC
QY 733 TGCAGAGCAGTTCAATCATACCAATGGTCTAAGTTTGGTTGACCGTGTCT
Db 666 CGCTACTCAGTTTAAACACACCAATGGACTCTCTCTGATTTCAAGAGCA
QY 793 GATGGAAGGATACAAATGGTGTGCGAGGATAAATGTGTGTCAAGTTTTCF
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QY 853 TTACTGTTTACCGTGTGGGAACATGGCCGCGCATATGAGATAGATGA
Db 786 CTATTGCTACCGTGTGCGCAACATGGCTGCGCATTTCTAGAGATCGGTGAGF
QY 913 GTCTTTTCTTCAAGTTCGAACACGACCGCGGCAAGTGAACCCAGATGTGA
Db 846 GAAATTTCTTCAAGTTTGTATCCAGCTCCAGCTCCAGTCCGAACCCGAACCA
QY 973 TCCTGATTAATTTCTGTAA 991
Db 906 TCCAGATTATTTTGTAA 924
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Job time : 1081 secs

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 07:11:40 ; Search time 242 Seconds
(without alignments)
2108.725 Million cell updates/sec

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Perfect score: 1365

Sequence: 1 ggcgttaacgcgcggaggag.....tatggcagctcgagctgcg 1365

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.*
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2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
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8: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq2.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	46.6	3.4	1864	6	US-10-750-185-37665
3	36.6	2.7	1861	6	US-10-750-185-62270
4	36	2.6	903	7	US-11-074-176-361
5	36	2.6	924	7	US-11-074-176-253
6	34.4	2.5	7292	7	US-11-075-646-5
7	34.2	2.5	2569	6	US-10-750-185-63345
8	34	2.5	175023	7	US-11-121-086-18
9	33.8	2.5	166639	7	US-11-121-086-52
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11	32.8	2.4	3156	6	US-10-750-185-46888
12	32.8	2.4	124972	7	US-11-121-086-100
13	32.8	2.4	134174	7	US-11-121-086-99
14	32.6	2.4	1614	7	US-11-167-856-21
15	32.6	2.4	1721	6	US-10-750-185-62692
16	32.6	2.4	2480	6	US-10-750-185-25218
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18	32.2	2.4	949	6	US-10-750-185-55420
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20	32.2	2.4	319608	7	US-11-145-703-1
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C 26	31.6	2.3	1470	6	US-10-750-185-42558	Seq
C 27	31.6	2.3	1557	6	US-10-750-185-41027	Seq
C 28	31.6	2.3	173602	7	US-11-121-086-25	Seq
C 29	31.4	2.3	828	6	US-10-467-657-2501	Seq
C 30	31.4	2.3	963	6	US-10-467-657-2503	Seq
C 31	31.4	2.3	95223	7	US-11-117-187-188	Seq
C 32	31.4	2.3	1082144	7	US-11-117-187-211	Seq
C 33	31.2	2.3	193789	7	US-11-112-908-55	Seq
C 34	31	2.3	1685	6	US-10-750-185-56877	Seq
C 35	31	2.3	1901	6	US-10-750-185-35821	Seq
C 36	31	2.3	2242	6	US-10-750-185-54495	Seq
C 37	31	2.3	2730	6	US-10-750-185-52345	Seq
C 38	31	2.3	125552	7	US-11-121-086-1	Seq
C 39	30.8	2.3	1200	9	US-11-082-389-343	Seq
C 40	30.8	2.3	2833	7	US-11-110-082-18	Seq
C 41	30.6	2.2	728	6	US-10-750-185-37667	Seq
C 42	30.6	2.2	1136	6	US-10-750-185-32673	Seq
C 43	30.6	2.2	189539	7	US-11-121-086-16	Seq
C 44	30.4	2.2	1149	6	US-10-750-185-42234	Seq
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ALIGNMENTS

RESULT 1

US-10-909-125-814

; Sequence 814, Application US/10909125

; Publication No. US20050261218A1

; GENERAL INFORMATION:

; APPLICANT: Esau, Christine

; APPLICANT: Lollo, Bridget

; APPLICANT: Bennett, C. Frank

; APPLICANT: Freier, Susan M.

; APPLICANT: Griffey, Richard H.

; APPLICANT: Baker, Brenda F.

; APPLICANT: Vickers, Timothy

; APPLICANT: Marcusson, Eric G.

; APPLICANT: Koller, Eric

; APPLICANT: Swayze, Eric

; APPLICANT: Jain, Ravi

; APPLICANT: Bhat, Balkrishen

; APPLICANT: Peralta, Egen

; TITLE OF INVENTION: Oligomeric Compounds And Compositions For

; FILE REFERENCE: Of Small Non-Coding RNAs

; CURRENT APPLICATION NUMBER: US/10/909,125

; CURRENT FILING DATE: 2004-07-30

; PRIOR APPLICATION NUMBER: US 60/492,056

; PRIOR FILING DATE: 2003-07-31

; PRIOR APPLICATION NUMBER: US 60/516,303

; PRIOR FILING DATE: 2003-10-31

; PRIOR APPLICATION NUMBER: US 60/531,596

; PRIOR FILING DATE: 2003-12-19

; PRIOR APPLICATION NUMBER: US 60/562,417

; PRIOR FILING DATE: 2004-04-14

; NUMBER OF SEQ ID NOS: 2184

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 814

; LENGTH: 1541

; TYPE: DNA

; ORGANISM: H. sapiens

; US-10-909-125-814

Query Match 37.5%; Score 512.4; DB 6; Length 15

Best Local Similarity 71.9%; Pred. No. 4e-161;

Matches 669; Conservative 0; Mismatches 261; Indels 3 0;

QY 86 GATGTAGACCGGACATAGACAGCTGCGAGTGCAAGCGGTGTCGGF

DB 46 GAGCTGGACGAGTGGTCTGACGAGCTGAACGAGTGTAGCAGCTGAACGF

IG 145

IG 105

```

QY 146 AAGAACCTATGTGATCAAGCTCGGACGATCTTGGTGGAGAGTGGAACGTGAGCCCGTG 205
Db 106 CGGACGCTGTGCGAGAGGCAAGGAAATTTTAAACAAAGAAATCAATGTGCAAGAGTT 165
QY 206 AAGTGTCTGTGACGAGTTTGGGTGACATCCATGCGCAGTTTCATGATCTCATGAGCTT 265
Db 166 CGTTCGCCCTGTACTGTCTGTGGAGATGTGCATGTGCAATTTTCATGATCTTATGGAATC 225
QY 266 TTCCCGCATAGGAGGCAAGCGCCGACACGAACTACTTGTTCATGGCGCACTATGTGGAT 325
Db 226 TTGAATTTGGTGGAAATCACCGGATACAACTACTTATTTCATGGGTGACTATGTAGAC 285
QY 326 CGTGGATATTAATCTGTGCGAGACTGTGCGCTTTAGTGGCCCTGAAGTGGCGGTATAGG 385
Db 286 AGAGGATATTAATTCAGTGAGACTGTGACTCTTCTGTAGCATTAAGAGTGGCTTATCCA 345
QY 386 GATAGATCACAATCTTGGAGGGAACACGAGAGCAGGCAATTAACCAAGTATATGGT 445
Db 346 GAAACGATTAACAATATTGAGAGGAATCACGAAAGCCGACAAATTAACCAAGTATATGGC 405
QY 446 TTCTATGATGAATGCTCGGGAAGTATGGAATGGCAATGTTTGGAAAGTACTTTCACGGAT 505
Db 406 TTTTATGATGAATGTCTGGAAGATGGGAATGCCAGCTTGGAAATATTTACAGAT 465
QY 506 CTGTTGGACTACCTGCTGTGACAGCTCTCATGTGACGAGATTTTGTCTTCATGGT 565
Db 466 CTCTTTGATTAATCTTCCACTTACAGCTTAGTATGAGATGGAAGATATCTGCTCCATGGT 525
QY 566 GGTCTGTCTCCATCGCTCGACATATAGATACATCCGAGCCCTAGATCGTATCAAGAA 625
Db 526 GGCCTCTCTCCATCCATGACACATGGAATCATATAAGAGCCCTGGATCGTTTACAGGAA 585
QY 626 GTGCGCGACAGGCGCGGATGTGATCTACTCTGCTGTGATCCAGATGATCGTTGTGGA 685
Db 586 GTTCACATAGGCGCCCAATGTGATCTGTTATGTCAGATCCAGATGATCGTGTGGA 645
QY 686 TGGGCGATTTCACAGAGGTGCCGTTATATCTTTTGGTCAAGATATTGACAGAGCTTC 745
Db 646 TGGGCTATTTCACAGCTGTGCTGCTACACATTTGGACAGACATTTCTGAAACCTTT 705
QY 746 AATCATACAAATGGTCTAAGTTTGGTGTGACGCTGTCCACAGCTTGTGATGGAAGATAC 805
Db 706 AACCATGCCAATGGTCTACACTGGTCTGCTGCGCCACACAGCTTGTAAATGGAGGATAC 765
QY 806 AATTGTGTCAGGATAAATGTTGTACAGTTTTCAGTGCCCCCAATTTACTGTTACGCG 865
Db 766 AATTGTGTCATGTCGGAATGGTTACCAATTTTCAGTGACCCCAATTTACTGTTATGCT 825
QY 866 TGTGGAAACATGCGCCCAATAATGGAGATAGATGAACAAATGAATCGGCTTTTCTTCAG 925
Db 826 TGTGGAAACAGGCTGCTATCATGGAATTTAGATGACACTTTAAATATTTCTCTCTCAA 885
QY 926 TTCGAACAGACGCGCGGCAAGTGAACAGATGTGACCGGGAAGACTCTCGAATTAATTT 985
Db 886 TTTGACCGCGCGCTGCTGCTGAGGCTCATGTTACACGCGCAGCCACCCAGACTACTTC 945
QY 986 CTGTAACATGCGCTATATACATGTTACTTTT 1015
Db 946 CTATAAATTTCTCTGGGAAACCTGCTTTT 975

```

RESULT 2

```

US-10-750-185-37665
; Sequence 37665, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen

```

```

; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37665
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Bovine 19866880394924
; US-10-750-185-37665

```

```

Query Match 3.4%; Score 46.6; DB 6; Length 196
Best Local Similarity 64.2%; Pred. No. 6.1e-05;
Matches 70; Conservative 0; Mismatches 39; Indels 0;

```

```

QY 496 CTTTACCGATCTGTTCCAGTACCTCTGACAGCTCTCATTTGAGCAGC 555
Db 1050 CTGCATGGATGCCCTTTGACTGCTGCCCTGGCTGATGAACCCAG 1109

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QY 556 TCTTCATGGTGTCTGTCTCCATCGCTCGACACATTAGATCACATCCGA 1110
Db 1110 GTGTCACGGCGTTTGTTCTCCAGAGATAAACACTTTAGATGATATCAGA

```

RESULT 3

```

US-10-750-185-62270
; Sequence 62270, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 62270
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Bovine 19866880123096
; US-10-750-185-62270

```

```

Query Match 2.7%; Score 36.6; DB 6; Length 186
Best Local Similarity 65.1%; Pred. No. 0.13;
Matches 54; Conservative 0; Mismatches 29; Indels 0;

```

```

QY 229 TGACATCCATGGCCAGTTTCATGATCTCATCGAGCTTTTCGCGCATAGGAG 288
Db 1620 TGCCCTTTCTTTATAGTTTATGACCTTTGTGAACTGTTTCAGAACTGGAG 1679

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QY 289 CGACACGAACACTTGTGTTTCATGG 311
Db 1680 TGACACAACTACATATTTATGG 1702

```

RESULT 4

```

US-11-074-176-361
; Sequence 361, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.

```

```

; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(903)
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1201; GTP-binding protein Era
US-11-074-176-361

```

```

Query Match      2.6%; Score 36; DB 7; Length 903;
Best Local Similarity 48.1%; Pred. No. 0.13;
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 887 ATGGAGATAGATGAACAATGAATCGTCTTTTCTTCAGTTCGAACCCAGCACCGGCGCAA 946
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 ATTGGTATTGATGATTGCTCAATCAATCTAATAGTATTTACCAGCAGGACCACAATAT 531

QY 947 AGTGAACAGATGTCAGCGGGAAGTCTCTGATTAATCTTCTGTAACATGGCCTATACAT 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 TATGATGAGATCAGATCAGATCGTCTCTGTAATATTTTGGTTGCGAAGCTTATTCGA 591

QY 1007 GGTACCTTTTACTTACTGAATTTCTGTATAGTACACCTTCCATCGAAGCAGTTTGCCCC 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 592 GAACAAATTTTACGACTTACTTCTCAAGAAAGTTCACATGCTACTGCAAGTTGATGCGAT 651

QY 1067 TGAATGAAGATACCTCCCTCATGATCTAGTAGT 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 652 CAAATGAATAAGCATCAAAATGGTAAATTAGT 683

```

```

RESULT 5
US-11-074-176-253
; Sequence 253, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(924)

```

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1201; GTP-binding protein Era
US-11-074-176-253

Query Match      2.6%; Score 36; DB 7; Length 924;
Best Local Similarity 48.1%; Pred. No. 0.13;
Matches 102; Conservative 0; Mismatches 110; Indels 0;

QY 887 ATGGAGATAGATGAACAATGAATCGTCTTTTCTTCAGTTCGAACCCAGC 946
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 493 ATTGGTATTGATGATTGCTCAATCAATCTAATAGTATTTACCAGCAGC 552

QY 947 AGTGAACAGATGTCAGCGGGAAGTCTCTGATTAATCTTCTGTAACATG 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 553 TATGATGAGATCAGATCAGATCGTCTCTGTAATATTTTGGTTGCGAG 612

QY 1007 GGTACCTTTTACTTACTGAATTTCTGTATAGTACACCTTCCATGGAAGC 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 613 GAACAAATTTTACGACTTACTTCTCAAGAAAGTTCACATGCTACTGCGAGT 672

QY 1067 TGAATGAAGATACCTCCCTCATGATCTAGTAGT 1098
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 673 CAAATGAATAAGCATCAAAATGGTAAATTAGT 704

```

```

RESULT 6
US-11-075-646-5/c
; Sequence 5, Application US/11075646
; Publication No. US20050261223A1
; GENERAL INFORMATION:
; APPLICANT: Czech, Michael P.
; APPLICANT: Powelka, Aimee
; APPLICANT: Guilherme, Adilson L.
; APPLICANT: Cherniack, Andrew D.
; TITLE OF INVENTION: RI140 REGULATION OF DIABETES
; FILE REFERENCE: 17738-009001
; CURRENT APPLICATION NUMBER: US/11/075,646
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,677
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7292
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-075-646-5

```

```

Query Match      2.5%; Score 34.4; DB 7; Length 7292
Best Local Similarity 53.8%; Pred. No. 1.8;
Matches 71; Conservative 0; Mismatches 61; Indels 0;

QY 137 TTGGAGGTGAAGAACCCTATGTGATCAAGCTCGACGATCTTGGTGGAGG 196
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3064 TTAAATTCAGATCAATTTCTGCTAAATTCAGCTCTTCTCTGGTTAAGC 3005

QY 197 CAGCCCGTGAAGTGTCTGTCAACGGTTTGGCGTACATCCATGGCCAGT 256
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3004 CAGTACTTCTGGGCGACTGTGATTTGTTGACGATCAACAATGTTGTTT 2945

QY 257 ATCGAGCTTTTC 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2944 AAATGGATTTC 2933

```

```

RESULT 7
US-10-750-185-63345
; Sequence 63345, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.

```



```

RESULT 14
US-11-167-856-21/c
; Sequence 21, Application US/11167856
; Publication No. US20050268352A1
; GENERAL INFORMATION:
; APPLICANT: Nikolau, Basil J
; APPLICANT: Wurtele, Eve S
; APPLICANT: Oliver, David J
; APPLICANT: Behal, Robert
; APPLICANT: Schnable, Patrick S
; APPLICANT: Ke, Jinshan
; APPLICANT: Johnson, Jerry L
; APPLICANT: Allred, Carolyn C
; APPLICANT: Fatland, Beth
; APPLICANT: Lutziger, Isabelle
; APPLICANT: Wen, Tsui-Jung
; TITLE OF INVENTION: Materials and Methods for the Alteration
; TITLE OF INVENTION: Acetyl CoA Levels in Plants
; FILE REFERENCE: P2194USDIV-2
; CURRENT APPLICATION NUMBER: US/11/167,856
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 10/293,865
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/344,882
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/090,717
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent In. Ver. 3.1

```

```
; SEQ ID NO 21
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Arabidopsis Thaliana
US-11-167-856-21

Query Match      2.4%; Score 32.6; DB 7; Length 1614;
Best Local Similarity 49.1%; Pred. No. 2.6;
Matches 86; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 753 CCAATGGTCTAAGTTTGGTTGCACGTGCTCACAGCTTGATGGAAGATACAATTGGT 812
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1237 CCAAGATTTCATCTTGGTATATCTTCATATCCTCAGTGACATCTGCCAATATAGTTGGT 1178
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 813 GCCAGATAAAATGTGTACAGTCTTTCAGTGCCCCCAATTTACTGTTACCGCTGTGGGA 872
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1177 TGGATGAATATCCCTTTGCTCCAAATGGCTTTTCTCCAGTTAATAAGTGGCTCCTTCG 1118
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 873 ACATGCCGCCCAATATGGAGATAGATGAACAATGAATCGGTCTTTTCTTCAGTT 927
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1117 TTTTACCGTGTCTCAATGTAGATAGAATCTTCTCAAACTGTCTTTTATCCACTT 1063
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-10-750-185-62692
; Sequence 62692, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62692
; LENGTH: 1721
; TYPE: DNA
; ORGANISM: Bovine 1986680961460
US-10-750-185-62692

Query Match      2.4%; Score 32.6; DB 6; Length 1721;
Best Local Similarity 50.3%; Pred. No. 2.8;
Matches 80; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 975 CTGATTACTTTCTGTAAACATGCGCTATACATGGTACCTTTTACTTACTGAATTGTTCTG 1034
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1420 CTGAAAGTCAGTGAACATAAACAATGATACAGGTATTCATATACTCTCTGATTATA 1479
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1035 TATAGTCACCTTCCCATGGAAGCAGTTTGCCCTGAAATGAAGATACTCCCTCATGATCTAG 1094
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1480 TTCACCTTTTGATCAATGTAGGACAGTTGTCTAAGAATAAATAAATAGGTGATTGTTAG 1539
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1095 TAGTATGAAGTTATCTTTCTTTGAAGTGTGTTTCCCTTT 1133
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1540 AAGACTGAATTTGACTAGTCTTAGCTCTTTTATCCTTTT 1578
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


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OM protein - protein search, using sw model

Run on: December 9, 2005, 08:23:56 ; Search time 137 Seconds
(without alignments)
981.386 Million cell updates/sec

Title: US-10-764-259-13
Perfect score: 1670
Sequence: 1 MPYADVDRQIEQLSECKPL.....EPAPRQSPDVTRKTPDYFL 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	306	5	ABb77578 Physcomit
2	1670	100.0	306	6	ABg74203 P. patens
3	1549	92.8	306	6	ABp98034 Protein p
4	1547	92.6	306	6	ABp98039 Protein p
5	1522	91.1	306	3	ABg31595 Arabidops
6	1521	91.1	306	6	ABp98027 Protein p
7	1518	90.9	312	8	ADy24822 Plant ful
8	1514	90.7	306	3	ABg23794 Arabidops
9	1509	90.4	306	3	ABg40766 Zea mays
10	1508.5	90.3	307	6	ABp98036 Protein p
11	1508	90.3	306	3	ABg32348 Arabidops
12	1504	90.1	306	3	ABg36033 Zea mays
13	1495	89.5	307	3	ABg29592 Arabidops
14	1486	89.0	304	8	ADt56656 Plant pol
15	1468	87.9	292	3	ABg31596 Arabidops
16	1460	87.4	292	3	ABg23795 Arabidops
17	1460	87.4	292	3	ABg32349 Arabidops
18	1447	86.6	292	3	ABg29593 Arabidops
19	1427	85.4	309	4	ABg67626 Amino aci
20	1427	85.4	309	4	ABg67641 Amino aci
21	1427	85.4	309	4	ABg67447 Amino aci
22	1427	85.4	309	4	ABg67462 Amino aci
23	1427	85.4	309	6	AAE33198 Human PPP
24	1427	85.4	309	7	ADB85518 Human MTS

25	1427	85.4	309	7	ADC16730	Adc16
26	1427	85.4	309	7	ADe63503	Ad63
27	1427	85.4	309	7	ADe63505	Ad63
28	1427	85.4	309	7	ADD45927	Ad45
29	1427	85.4	309	8	ADD45925	Ad45
30	1427	85.4	309	8	ADL83148	Adl83
31	1427	85.4	309	9	ADX05674	Adx05
32	1427	85.4	309	9	ADY70515	Ady70
33	1427	85.4	309	9	ADY97844	Ady97
34	1411	84.5	309	5	AAO22786	AO222
35	1411	84.5	309	5	AAO22787	AO222
36	1411	84.5	309	5	ABBS7104	ABBS7
37	1411	84.5	309	6	AAE33199	AAE33
38	1411	84.5	309	6	AAE33200	AAE33
39	1411	84.5	309	7	ADB85517	ADB85
40	1411	84.5	309	7	ADC16729	Adc16
41	1411	84.5	309	8	ADJ66518	Adj66
42	1411	84.5	309	8	ADJ66518	Adj66
43	1411	84.5	309	9	ADX08187	Adx08
44	1411	84.5	309	9	ADY70516	Ady70
45	1408	84.3	314	6	ABP98035	ABp98

ALIGNMENTS

RESULT 1
ABb77578
ID ABb77578 standard; protein; 306 AA.
XX
XX
AC ABb77578;
XX
DT 02-SEP-2002 (first entry)
XX
DE Physcomitrella patens PP2A-4 SEQ ID NO 13.
XX
XX
KW Physcomitrella patens; PHSRP; phosphatase stress related pr
KW PP2C; enzyme; transgenic; plant; stress tolerance.
XX
XX
OS Physcomitrella patens.
XX
XX
FN WO200246442-A2.
XX
XX
PD 13-JUN-2002.
XX
XX
PF 06-APR-2001; 2001WO-US011253.
XX
XX
PR 07-APR-2000; 2000US-0196001P.
XX
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
XX
PI Da Costa E SilvaO, Bohnert HJ, Ishitani M, Van Thielens N
XX
XX
DR WPI; 2002-508562/54.
DR N-PSDB; ABN81332.
XX
XX
PT New transgenic plant cell transformed by phosphatase stress
PT protein coding nucleic acid whose expression in the cell re
PT increased tolerance to environmental stress compared to wil
XX
XX
PS Claim 16; Fig 3; 106pp; English.
XX
XX
CC The invention relates to a transgenic plant cell (I) transf
CC phosphatase stress-related protein (PHSRP) coding nucleic a
CC ABN81334), where expression of the nucleic acid in the plan
CC in increased tolerance to an environmental stress as compar
CC type variety of the plant cell. PHSRP encoding genes are us
CC identifying Physcomitrella patens and related organisms, as
CC specific regions of the genome, mapping of genomes of organ
CC to P. patens, identification and localisation of P. patens
CC interest, evolutionary studies, determination of PHSRP regi
CC for function, modulation of a PHSRP activity, modulation of the
CC metabolism of one or more cell functions, modulation of the

CC transport of one or more compounds and modulation of stress resistance.
CC The gene is also useful for identifying and/or cloning PHSRP homologues
CC in other cell types and organisms, for identifying an organism as being
CC P. patens or its close relative and for evolutionary and protein
CC structural studies. The present sequence is that of a PHSRP of the
CC invention
XX
SQ Sequence 306 AA;
Query Match 100.0%; Score 1670; DB 5; Length 306;
Best Local Similarity 100.0%; Pred. No. 7.7e-165;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEENWVQPKCPVTTCGDIHGQFH 60
DB 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEENWVQPKCPVTTCGDIHGQFH 60
QY 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALLVKVRYDRITILRGHESRQI 120
DB 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALLVKVRYDRITILRGHESRQI 120
QY 121 TQVYGFYDECLRKYGNNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRAL 180
DB 121 TQVYGFYDECLRKYGNNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRAL 180
QY 181 DRIQVPHGPMCDLLWSDDPDRCCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240
DB 181 DRIQVPHGPMCDLLWSDDPDRCCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240
QY 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPQSEPDVTRK 300
DB 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPQSEPDVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306
RESULT 2
ABG74203
ID ABG74203 standard; protein; 306 AA.
AC ABG74203;
XX
XX 08-APR-2003 (first entry)
XX P. patens protein phosphatase PP2A-4.
XX Plant; enzyme; PP2A-4; protein phosphatase; PHSRP; cold; transgenic;
KW phosphatase stress related protein; environmental stress; drought;
KW salt tolerance.
XX Physcomitrella patens.
OS
XX
XX US2002152502-A1.
XX 17-OCT-2002.
XX 06-APR-2001; 2001US-00828302.
XX 07-APR-2000; 2000US-0196001P.
XX (SILV/) DA COSTA E SILVA O.
PA (BOHN/) BOHNERT H J.
PA (VTHI/) VAN THIELEN N.
PA (CHEN/) CHEN R.
PA (ISHI/) ISHITANI M.
XX Da Costa E SilvaO, Bohnert HJ, Van Thielen N, Chen R, Ishitani M;
PI WPI; 2003-198392/19.
XX DR N-PSDB; ABX16239.
XX

PT New transgenic plant cell transformed by a Phosphatase Stre:
PT Protein (PHSRP) coding nucleic acid, useful for modifying s
XX tolerance of a plant.
XX Claim 16; Fig 3C; 79pp; English.
XX
CC The invention relates to a transgenic plant cell transforme
CC Phosphate Stress-Related Protein (PHSRP) coding nucleic a
CC expression of the nucleic acid in the plant cell results in
CC tolerance to an environmental stress (e.g. salt tolerance, (t
CC drought) as compared to a wild type variety of the plant ce
CC include are a transgenic plant comprising the novel plant c
CC produced by the transgenic plant of (where the seed is true
CC an increased tolerance to environmental stress as compared
CC variety of the plant cell, an agricultural product produce
CC or seed, an isolated PHSRP or PHSRP coding nucleic acid, a
CC expression vector comprising the nucleic acid, and produc
CC plant containing PHSRP nucleic acid. The transgenic plant c
CC transformed by a Phosphatase Stress-Related Protein (PHSRP)
CC nucleic acid is useful for modifying stress tolerance of a
CC present sequence represents the PHSRP, protein phosphatase,
XX Sequence 306 AA;
SQ
Query Match 100.0%; Score 1670; DB 6; Length 30
Best Local Similarity 100.0%; Pred. No. 7.7e-165;
Matches 306; Conservative 0; Mismatches 0; Indels
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEENWVQPKCPVT
DB 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEENWVQPKCPVT
QY 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALLVKVRYDRITI
DB 61 DLIELFRIGGKAPDNTNLYFMGDYVDRGYYSVETVSLVALLVKVRYDRITI
QY 121 TQVYGFYDECLRKYGNNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPS
DB 121 TQVYGFYDECLRKYGNNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPS
QY 181 DRIQVPHGPMCDLLWSDDPDRCCGWGISPRGAGYTFGQDIAEQFNHTNG
DB 181 DRIQVPHGPMCDLLWSDDPDRCCGWGISPRGAGYTFGQDIAEQFNHTNG
QY 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAP
DB 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAP
QY 301 TPDYFL 306
DB 301 TPDYFL 306
RESULT 3
ABP98034
ID ABP98034 standard; protein; 306 AA.
XX
XX AC ABP98034;
XX
XX 11-AUG-2003 (first entry)
XX Protein phosphatase stress-related polypeptide GmPP2A-5.
DE
XX Protein phosphatase stress-related polypeptide; PHSRP; PPPP
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;
KW drought; salinity; cold; enzyme.
XX Glycine max.
XX WO2003020914-A2.
XX 13-MAR-2003.
PD

XX 05-SEP-2002; 2002WO-US028445.
XX 05-SEP-2001; 2001US-0317305P.
XX (BADI) BASF PLANT SCI GMBH.
XX Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa E Silva O;
XX WPI; 2003-300886/29.
XX N-PSDB; ACC43349.
XX New protein phosphatase stress-related polypeptide coding nucleic acid,
XX useful for modulating plant's tolerance to an environmental stress such
XX as drought, increased salinity and cold.
XX Claim 14; Page 82-83; 107pp; English.
XX The present sequence represents a protein phosphatase stress-related
XX polypeptide (PPSRP). The specification describes PPSRP polypeptides
XX designated Pp2A-1, Pp2A-2, BnPP2A-1, BnPP2A-2, GmPP2A-1,
XX GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from
XX Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP
XX polypeptides and polynucleotides are useful for modulating plant
XX tolerance to an environmental stress such as drought or increased
XX salinity and cold. They are also useful in identification and
XX localization of Physcomitrella patens, Brassica napus, Glycine max or
XX Oryza sativa and related organisms, mapping of genomes of organisms
XX related to the above species, in a evolutionary and polypeptide
XX structural studies, in determination of PPSRP regions required for
XX function, modulation of PPSRP activity, modulation of metabolism of one
XX or more cell functions and transmembrane transport of one or more
XX components
XX Sequence 306 AA;
Query Match 92.8%; Score 1549; DB 6; Length 306;
Best Local Similarity 91.5%; Pred. No. 3.1e-152;
Matches 280; Conservative 16; Mismatches 10; Indels 0; Gaps 0;
QY 1 MPSADVDRQIEQLSECKPLSEVKNLCOARTILVEENWVQPKCVTVCGDIHQGFH 60
DB 1 MPESHADLERQIEQLMDCKPLSEVKALCDQARTILVEENWVQPKCVTVCGDIHQGFY 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVSETVSLVALLVVKVYRDRTITLGRNHESRQI 120
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVSETVTLVALLVVKVYRDRTITLGRNHESRQI 120
QY 121 TQVGYFYDECLRKYGNNVWKFYTDLDYFLPLTALIEHIEIFCLHGLSPSLDTLDHIAL 180
DB 121 TQVGYFYDECLRKYGNNVWKFYTDLDYFLPLTALIEHIEIFCLHGLSPSLDTLDHIAL 180
QY 181 DRIQEVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNG 240
DB 181 DRIQEVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNG 240
QY 241 VMGYNMCDKNVTVFSAFNPCYRCGNMAAIMEIDETMNSFLOFEPAPQSEPDVTRK 300
DB 241 VMGYNMCDKNVTVFSAFNPCYRCGNMAAIMEIDETMNSFLOFEPAPQSEPDVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306
RESULT 4
ID ABP98039
XX ABP98039 standard; protein; 306 AA.
XX AC ABP98039;
XX 11-AUG-2003 (first entry)
XX

DE Protein phosphatase stress-related polypeptide OsPP2A-5.
XX Protein phosphatase stress-related polypeptide; PPSRP; Pp2A-1;
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;
KW drought; salinity; cold; enzyme.
XX Oryza sativa.
XX WO2003020914-A2.
XX 13-MAR-2003.
XX 05-SEP-2002; 2002WO-US028445.
XX 05-SEP-2001; 2001US-0317305P.
XX (BADI) BASF PLANT SCI GMBH.
XX Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa
XX WPI; 2003-300886/29.
XX N-PSDB; ACC43354.
XX New protein phosphatase stress-related polypeptide coding r
XX useful for modulating plant's tolerance to an environmental
XX as drought, increased salinity and cold.
XX Claim 18; Page 88; 107pp; English.
XX The present sequence represents a protein phosphatase stress
XX polypeptide (PPSRP). The specification describes PPSRP poly
XX designated Pp2A-1, Pp2A-2, BnPP2A-1, BnPP2A-2, BnPP2A-3,
XX GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived
XX Physcomitrella patens, Brassica napus, Glycine max or Oryza
XX polypeptides and polynucleotides are useful for modulating
XX tolerance to an environmental stress such as drought or inc
XX salinity and cold. They are also useful in identification a
XX localization of Physcomitrella patens, Brassica napus, Glyc
XX Oryza sativa and related organisms, mapping of genomes of c
XX related to the above species, in a evolutionary and polypep
XX structural studies, in determination of PPSRP regions requi
XX function, modulation of PPSRP activity, modulation of metat
XX or more cell functions and transmembrane transport of one c
XX components
XX Sequence 306 AA;
Query Match 92.6%; Score 1547; DB 6; Length 306
Best Local Similarity 91.5%; Pred. No. 5e-152;
Matches 280; Conservative 15; Mismatches 11; Indels
QY 1 MPSADVDRQIEQLSECKPLSEVKNLCOARTILVEENWVQPKCVTV
DB 1 MPESHADLERQIEQLMECKPLSEVKNLCOARTILVEENWVQPKCVTV
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVSETVSLVALLVVKVYRDRTIT
DB 61 DLIELFRIGGNAPDNTNLFMGDYVDRGYVSETVTLVALLVVKVYRDRTIT
QY 121 TQVGYFYDECLRKYGNNVWKFYTDLDYFLPLTALIEHIEIFCLHGLSPSE
DB 121 TQVGYFYDECLRKYGNNVWKFYTDLDYFLPLTALIEHIEIFCLHGLSPSE
QY 181 DRIQEVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNG
DB 181 DRIQEVPEHGMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNG
QY 241 VMGYNMCDKNVTVFSAFNPCYRCGNMAAIMEIDETMNSFLOFEPAF
DB 241 VMGYNMCDKNVTVFSAFNPCYRCGNMAAIMEIDETMNSFLOFEPAF
QY 301 TPDYFL 306

PP-1;
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PPSRP

or

one

-s 0;

PF 60

PF 60

QI 120

QI 120

AL 180

AL 180

QL 240

QL 240

RK 300

RK 300

Query Match 91.1%; Score 1521; DB 6; Length 306;
Best Local Similarity 88.9%; Pred. No. 2.5e-149;
Matches 272; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEENWVQPKVPTVCGDIHGQPH 60
DB 1 MPETGDIQRIEQLMECKALSAEVTICEQRAILVEENWVQPKVPTVCGDIHGQFY 60

QY 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLVALLKVRVDRITILRGNHESRQI 120
DB 61 DLIELFKIGGSPDTNYLFMGDYVDRGYYSVETVSLVALLKVRVDRITILRGNHESRQI 120

QY 121 TQVYGFYDECLRKYGKGNANWKYFTDLYPLPTALIEHIFCLHCGLSPLDTHIRAL 180
DB 121 TQVYGFYDECLRKYGKGNANWKYFTDLYPLPTALIESQVFCFHGGLSPSLDTLNIHSL 180

QY 181 DRIQVPEHGPWCDDLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSVARAHQL 240
DB 181 DRIQVPEHGPWCDDLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSVARAHQL 240

QY 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSLFQFEPAPRQSEPDVTRK 300
DB 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAILEIDENMQNLFQDPAPRQVEPETTRK 300

QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 7
ADY24822
ID ADY24822 standard; protein; 312 AA.

XX AC ADY24822;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polypeptide seqid 72606.

XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content.
XX OS Unidentified.

XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIU/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABA/) TABASKA J E.
XX PA (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.
XX Claim 1; SEQ ID NO 72606; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The purpose of the invention are also useful in physical arrays of molecular plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, osmotic conditions, pathogens or pests, for manipulating growth of plant cells by modification of the cell cycle pathway, for increasing resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use, or by providing improved plant growth and development under stress condition or for modifying seed oil or protein yield content. This is the amino acid sequence of a plant full length polypeptide that can be used in the recombinant DNA construct invention.

XX SQ Sequence 312 AA;

Query Match 90.9%; Score 1518; DB 8; Length 312
Best Local Similarity 88.9%; Pred. No. 5.4e-149;
Matches 272; Conservative 23; Mismatches 11; Indels 0;

QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEENWVQPKVPTV 60
DB 7 MPSHADLDHQISQLRDCKFLPEVEVKLCEKAKAILMEENWVQVRCPV 66

QY 61 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLVALLKVRVDRITIL 120
DB 67 DLIELFRIGGKAPDTNYLFMGDYVDRGYYSVETVSLVALLKVRVDRITIL 126

QY 121 TQVYGFYDECLRKYGKGNANWKYFTDLYPLPTALIEHIFCLHCGLSPLS 180
DB 127 TQVYGFYDECLRKYGKGNANWKYFTDLYPLPTALIEHIFCLHCGLSPLS 186

QY 181 DRIQVPEHGPWCDDLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG 240
DB 187 DRIQVPEHGPWCDDLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG 246

QY 241 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSLFQFEPAP 300
DB 247 VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAILEIDENMQNLFQDPAP 306

QY 301 TPDYFL 306
DB 307 TPDYFL 312

RESULT 8
AAG23794
ID AAG23794 standard; protein; 306 AA.

XX AC AAG23794;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 27233.
XX KW Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.
 PF 25-FEB-1999; 99US-0121825P.
 XX 25-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126785P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-0130449P.
 PR 23-APR-1999; 99US-0130510P.
 PR 28-APR-1999; 99US-0130891P.
 PR 30-APR-1999; 99US-0131449P.
 PR 30-APR-1999; 99US-0132048P.
 PR 03-MAY-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132484P.
 PR 05-MAY-1999; 99US-0132485P.
 PR 06-MAY-1999; 99US-0132486P.
 PR 07-MAY-1999; 99US-0132487P.
 PR 11-MAY-1999; 99US-0132566P.
 PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134221P.
 PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135623P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 21-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
 PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 20-JUL-1999; 99US-0144844P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145085P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145192P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145913P.
 PR 27-JUL-1999; 99US-0145918P.
 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145951P.
 PR 02-AUG-1999; 99US-0146386P.
 PR 02-AUG-1999; 99US-0146388P.
 PR 02-AUG-1999; 99US-0146389P.
 PR 03-AUG-1999; 99US-0147038P.
 PR 04-AUG-1999; 99US-0147204P.
 PR 04-AUG-1999; 99US-0147302P.
 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147493P.
 PR 09-AUG-1999; 99US-0147935P.
 PR 10-AUG-1999; 99US-0148171P.
 PR 11-AUG-1999; 99US-0148319P.
 PR 12-AUG-1999; 99US-0148341P.
 PR 13-AUG-1999; 99US-0148565P.
 PR 16-AUG-1999; 99US-0148684P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 23-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149910P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151030P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.

PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
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PR 22-OCT-1999; 99US-0160980P.
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PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
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PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162143P.

Query Match 90.7%; Score 1514; DB 3; Length 306;

Best Local Similarity 89.2%; Pred. No. 1.4e-148;

Matches 273; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 MPSYADVDRQTEQLSECKPLSELVKNLQDQARTILVEENNVPVKCPVTTCGDIHGQFH 60
DB 1 MFSNGDLDRDTEQLMECKPLGEADYKILCDQAKAILVEEYNNVPVKCPVTTCGDIHGQFY 60
QY 61 DLIELFRIGGRKAPDNYLFMGDYVDRGYVSVETVLLVALKVYRDRITILRGNHESQI 120
DB 61 DLIELFRIGGRKAPDNYLFMGDYVDRGYVSVETVLLVALKVYRDRITILRGNHESQI 120
QY 121 TQVYGFYDECLRKYGANVWKYFTDLFDYLPALTALIEHIFCLHGLSPSLDTLPHIRAL 180
DB 121 TQVYGFYDECLRKYGANVWKYFTDLFDYLPALTALIESQVFLHGLSPSLDTLDIRSL 180
QY 181 DRIOQVHEGPMCDLLWSDPDDRCWGGISPRCAGYTFQODIABQFNHTNGILSVARAHQL 240
DB 181 DRIOQVHEGPMCDLLWSDPDDRCWGGISPRCAGYTFQODIATQFNHNHGLSLISRAHQL 240
QY 241 VMEGYNWQDKNNVTVFSAFNPCYRCGNMAAIMEIDETWNRSLFQEPAPROSEPDVTRK 300
DB 241 VMEGYNWQDKNNVTVFSAFNPCYRCGNMAAILEIGKEQNFLOFDPAPRQVEPDVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 9
AAG40766
ID AAG40766 standard; protein; 306 AA.
XX
AC AAG40766;
XX

DT 18-OCT-2000 (first entry)
XX Zea mays protein fragment SEQ ID NO: 50628.
DE Protein identification; signal transduction pathway; metabo-
vay;
KW hybridisation assay; genetic mapping; gene expression contr-
vay;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
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PR 18-JUN-1999; 99US-0139457P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.

PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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Db 241 VMEGFNWCQDKNVTVFSAPNYCYRCGNMAAILIEIGENMDQNFLOQDPAPRQIEPDTRK 300

Qy 301 TPDYFL 306
|||||

Db 301 TPDYFL 306

RESULT 10
ABP98036
ID ABP98036 standard; protein; 307 AA.

XX AC ABP98036;
XX DT 11-AUG-2003 (first entry)
XX DE Protein phosphatase stress-related polypeptide OsPP2A-2.
XX KW Protein phosphatase stress-related polypeptide; PPSRP; PpPP2A-1; PpPP-1;
KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3; OsPP2A-1;
KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress; plant;
KW drought; salinity; cold; enzyme.
XX OS Oryza sativa.
XX PN WO2003020914-A2.
XX XX 13-MAR-2003.
XX PF 05-SEP-2002; 2002WO-US028445.
XX PR 05-SEP-2001; 2001US-0317305P.
XX PA (BADI) BASF PLANT SCI GMBH.
XX PI Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa E SilvaO;
XX WPI; 2003-300886/29.
DR N-PSDB; ACC43351.
XX

New protein phosphatase stress-related polypeptide coding nucleic acid, useful for modulating plant's tolerance to an environmental stress such as drought, increased salinity and cold.

Claim 16; Page 85; 107pp; English.

The present sequence represents a protein phosphatase stress-related polypeptide (PPSRP). The specification describes PPSRP polypeptides designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, GmPP2A-1, GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP polypeptides and polynucleotides are useful for modulating plant tolerance to an environmental stress such as drought or increased salinity and cold. They are also useful in identification and localisation of Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa and related organisms, mapping of genomes of organisms related to the above species, in a evolutionary and polypeptide structural studies, in determination of PPSRP regions required for function, modulation of PPSRP activity, modulation of metabolism of one or more cell functions and transmembrane transport of one or more components

XX Sequence 307 AA;

Query Match 90.3%; Score 1508.5; DB 6; Length 307;
Best Local Similarity 88.6%; Pred. No. 5.1e-148;
Matches 272; Conservative 23; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MP-SYADVDRQIEQSECKPSELEVNKLCDOARTILVEENVQVPCVTVCGDIHQGF 59
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MPSSGGLDRQIAQRECKHLAGSEVRALCEQAKILMEENVQVPCVTVCGDIHQGF 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 HDLIELFRIGGKAPDNTYLFMGDYVDRGYSVETVSLVALKVRYRDRITLRGNHESRQ 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 YDLIELFRIGGEAPDNTYLFMGDYVDRGYSVETVSLVALKVRYRDRIT

Qy 120 ITQVYGFYDECLRKYGNAVWKYFTDLFDYLPPLALIEHEIFCLHGGLSLP;
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 121 ITQVYGFYDECLRKYGNAVWKYFTDLFDYLPPLALIEHQVFCVCLHGGLSLP;
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 180 LDRIQEVPHGPMCDLLWSDPDDRCGNGISPRGAGYTFGODIAEQFNHTN;
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 181 LDRIQEVPHGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAQQFNHTN;
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 240 LVMEGYNWCQDKNVTVFSAPNYCYRCGNMAAILIEIDETMNRSLQPEPA;
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 241 LVMEGFNWCQDKNVTVFSAPNYCYRCGNMAAILIEIGENMDQNFLOQDPAP;
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 300 KTPDYFL 306
|||||

Db 301 KTPDYFL 307

RESULT 11
AAG32348
ID AAG32348 standard; protein; 306 AA.

XX AC AAG32348;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 39006.
XX KW Protein identification; signal transduction pathway; metabo-
KW hybridisation assay; genetic mapping; gene expression contr-
KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
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PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
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PR 25-MAY-1999; 99US-0136021P.
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PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
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PR 24-JUN-1999; 99US-0140823P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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PR 13-JUL-1999; 99US-0143542P.
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Query Match          90.3%; Score 1508; DB 3; Length 306;
Best Local Similarity 88.9%; Pred. No. 5.8e-148;
Matches 272; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

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QY 61 DLIELFRIGGKAPDNYLFMGDYVDRGYVETVSLVALKVYRDRITILRGNHESRQI 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DLIELFRIGGKAPDNYLFMGDYVDRGYVETVSLVALKVYRDRITILRGNHESRQI 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 TQVGYFDECLRKYGNNANWKYFTDLFDYLPITALIEHIEIFCLHGLSPSLDTLPHIRAL 180
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Db 121 TQVGYFDECLRKYGNNANWKYFTDLFDYLPITALIESQVFCFHGLSPSLDTLDNIRSL 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 DRIQVPHGPMCDLLWSDPDDRCWGISPRGAGYTFQODIABQFNHTNGLSLVARAHQL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 DRIQVPHGPMCDLLWSDPDDRCWGISPRGAGYTFQODIATQFNHNHGLSLISRAHQL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 VNEGYNWQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSRPDVTRK 300
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Db 241 VNEGYNWQCKNNVTVFSAPNYCYRCGNMAALIEIGKMEQNFLQFDPAPRQVEPDTRK 300
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QY 301 TPDYFL 306
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Db 301 TPDYFL 306
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RESULT 12
AAG36033
ID AAG36033 standard; protein; 306 AA.
AC AAG36033;
XX
XX 18-OCT-2000 (first entry)
XX
XX Zea mays protein fragment SEQ ID NO: 44102.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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Query Match 90.1%; Score 1504; DB 3; Length 306
Best Local Similarity 87.9%; Pred. No. 1.5e-147;
Matches 269; Conservative 22; Mismatches 15; Indels

QY 1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENWVQVPCPV
DB 1 MPHGDLDRQIAQRDCCKYLPEAEVKVLCQAKILMEENWVQVPCPV

QY 61 DLIELFRIGGRKAPDTNYLFMGDYVDRGYYSVETVSLVALKVRDRIT
DB 61 DLIELFRIGGSDPTNYLFMGDYVDRGYYSVETVSLVALKVRDRIT

QY 121 TQYGFYDECLRKYGNANWVKYFTDLFDYLPALIEHIFCLHGGLSPE
DB 121 TQYGFYDECLRKYGNANWVKYFTDLFDYLPALIEHIFCLHGGLSPE

QY 181 DRIOEPHEGPMCDLLMSDDPDRCGWGISPRGAGVTGQDIAEQFNHTNG
DB 181 DRIOEPHEGPMCDLLMSDDPDRCGWGISPRGAGVTGQDIAEQFNHTNG

QY 241 VMEGYNQCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAF
DB 241 VMEGYNQCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAF

QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 13
AAG29592
ID AAG29592 standard; protein; 307 AA.
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AC AAG29592;
XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 35236.
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KW Protein identification; signal transduction pathway; metabo
KW hybridisation assay; genetic mapping; gene expression contr
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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Matches 268; Conservative 23; Mismatches 14; Indels 0; Gaps 0;

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Db 303 PDYFL 307
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RESULT 14
ADT56656
ID ADT56656 standard; protein; 304 AA.

AC ADT56656;

XX 13-JAN-2005 (first entry)

DE Plant polypeptide, SEQ ID 6733.

KW Plant; transgenic; cold tolerance; growth rate; drought tolerance;
KW disease resistance; galactomannan production; plant growth regulator;
KW heat tolerance; herbicide tolerance; lignin production;
KW extreme osmotic condition tolerance; pathogens resistance;
KW pest resistance; yield improvement; seed oil yield; seed protein yield.

XX Viridiplantae.
OS US2004216190-A1.
PN 28-OCT-2004.
PD 18-DEC-2003; 2003US-00739930.
PF 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX (KOVA/) KOVALIC D K.
XX Kovalic DK;
XX WPI; 2004-757369/74.
XX New recombinant DNA constructs useful in the field of bioch
PT Genetics, and in particular for producing transgenic plants
PT biological characteristics.

PS Claim 2; SEQ ID NO 6733; 14pp; English.

CC The invention relates a recombinant DNA construct comprising
CC polynucleotide having any of 5544 nucleotide sequences (CDN
CC 1-5544) and encoding a polypeptide with any of 5544 amino a
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from cc
CC Arabidopsis, wheat and rape but the specification does not
CC sequences is derived from which organism. Also included is
CC producing a plant having an improved property, comprising t
CC plant with a recombinant DNA construct comprising a promote
CC functional in a plant cell operably joined to a polynucleot
CC polypeptide associated with the property, and growing the t
CC plant. The property is selected from improving plant cold t
CC manipulating growth rate in plant cells by modification of
CC pathway, for improving plant drought tolerance, for providi
CC resistance to plant disease, for galactomannan production,
CC of plant growth regulators, for improving plant heat tolera
CC improving plant tolerance to herbicides, for increasing the
CC homologous recombination in plants, for lignin production,
CC plant tolerance to extreme osmotic conditions, for improv
CC tolerance to pathogens or pests, for yield improvement by n
CC photosynthesis, for modifying seed oil yield and/or content
CC modifying seed protein yield and/or content, for yield impr
CC modification of carbohydrate, nitrogen or phosphorus use ar
CC and for yield improvement by providing improved plant grow
CC development under at least one stress condition. The polyn
CC also encode a plant transcription factor. The methods and c
CC the present invention are useful in the field of biochemist
CC biological characteristics such as increased yield, improve
CC flow, increasing plant tolerance to cold or heat, improving
CC tolerance to extreme osmotic and drought conditions, and in
CC tolerance to plant pests or pathogens. They can also be use
CC arrays of molecules, plant breeding markers, computer-based
CC analysis systems. The present sequence is one of the 5544 f
CC sequences of the invention. Note: The sequence data for thi
CC not form part of the printed specification, but was obtaine
CC electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040216190.

XX Sequence 304 AA;

Query Match 89.0%; Score 1486; DB 8; Length 304
Best Local Similarity 88.2%; Pred. No. 1.1e-145;
Matches 270; Conservative 16; Mismatches 18; Indels

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PR 27-DEC-1999; 99US-0161999P.
PR 28-DEC-1999; 99US-0161999P.
PR 29-DEC-1999; 99US-0161999P.
PR 30-DEC-1999; 99US-0161999P.
PR 31-DEC-1999; 99US-0161999P.

Search completed: December 9, 2005, 10:20:24
Job time : 139 secs

s 0;
DT 75
DT 61
YG 135
YG 121
DL 195
DL 181
VT 255
VT 241

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Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	1522	91.1	306	2	S31162	phosphoprotein phospho
2	1508	90.3	306	2	S31161	phosphoprotein phospho
3	1501.5	89.9	305	2	S37086	phosphoprotein phospho
4	1495	89.5	307	1	B96722	phosphoprotein phospho
5	1481	88.7	306	2	T03389	probable phosphopr
6	1445	86.5	302	2	T03599	phosphoprotein phospho
7	1427	85.4	309	1	A27430	phosphoprotein phospho
8	1427	85.4	309	1	PAHU2A	phosphoprotein phospho
9	1427	85.4	309	1	PAREB1	phosphoprotein phospho
10	1427	85.4	309	1	PART2A	phosphoprotein phospho
11	1427	85.4	309	1	S10371	phosphoprotein phospho
12	1421	85.1	309	1	S20348	phosphoprotein phospho
13	1412	84.6	309	1	S12961	phosphoprotein phospho
14	1411	84.5	309	1	PAHU2B	phosphoprotein phospho
15	1411	84.5	309	1	PARE2B	phosphoprotein phospho
16	1411	84.5	309	1	PART2B	phosphoprotein phospho
17	1410	84.4	309	1	JC4316	phosphoprotein phospho
18	1388	83.1	318	1	T21975	phosphoprotein phospho
19	1386	83.0	313	1	S52660	phosphoprotein phospho
20	1385	82.9	308	2	S31163	phosphoprotein phospho
21	1385	82.9	313	1	S52659	phosphoprotein phospho
22	1377	82.5	293	2	B27430	phosphoprotein phospho
23	1375	82.3	313	1	S35502	phosphoprotein phospho
24	1367	81.9	322	2	B36076	phosphoprotein phospho
25	1360.5	81.5	314	2	T09596	phosphoprotein phospho
26	1358	81.3	309	2	S12986	phosphoprotein phospho
27	1346	80.6	314	2	T03600	phosphoprotein phospho
28	1328	79.5	309	2	A36076	phosphoprotein phospho
29	1328	79.5	325	2	A28029	phosphoprotein phospho

F;85,210/Binding site: substrate phosphate (Arg) #status predicted

```
Query Match          89.9%; Score 1501.5; DB 2; Length 307  
Best Local Similarity 88.2%; Pred. No. 3.5e-126;  
Matches 270; Conservative 21; Mismatches 14; Indels
```

QY 1 MPSYADVDRQIEQLSECKPLSELVKNLCDQAARTILVEEWNVPVKCPVT
| | | : | | | : | | | : | | | : | | | : | | |
Db 1 MPSQSDDRQIEHMDCKPLPE-EVRTCLDQAARTILVEEWNVPVKCPVT
| | | : | | | : | | | : | | | : | | | : | | |

QY 61 DLTELPRIGGKAPDTNYLFMGDVVDRGYSVETVSLIALVKVRDRDRIITL
| | | : | | | : | | | : | | | : | | | : | | |
Db 60 DLEELFRIGGSADPTNYLFMGDVVDRGYSVETVLLVALKVRYRDRITI
| | | : | | | : | | | : | | | : | | | : | | |

QY 121 TQVYGVFDECLRKYGNANWKKYFTDLFDYLPLTALTEHEIFLCFHGGLSPS:
| | | : | | | : | | | : | | | : | | | : | | |
Db 120 TQVYGFDFECLRKYGNANWKHTFDFLYLPALTLESQIFLCFHGGLSPS:
| | | : | | | : | | | : | | | : | | | : | | |

QY 181 DRIOEVHPHGMCDDLWSDDPDCGWGISPRGAGYTFGQDIASQFNHTNGI
| | | : | | | : | | | : | | | : | | | : | | |
Db 180 DRIOEVHPHGMCDDLWSDDPDCGWGISPRGAGYTFGQDIAAQFNHTNGI
| | | : | | | : | | | : | | | : | | | : | | |

QY 241 VMEGYNCWDQNKVTVVSAPNYCYRCGNMAAWEIDETMNRSLQFPAPAI
| | | : | | | : | | | : | | | : | | | : | | |
Db 240 VMEGYNWSQNNVVTFISAPNYCYRCGNMAALEVGENDQNFLOFPAPAI
| | | : | | | : | | | : | | | : | | | : | | |

QY 301 TPDPFL 306
| | | | |
Db 300 TPDPFL 305
| | | | |

RESULT 4

B96722

phosphoprotein phosphatase (EC 3.1.3.16) 2A catalytic chain F20P

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 1

C/Accession: B96722

R/Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.I.; Schwartz, J.R.; Shinn, P.; Southwick,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arab

A/Reference number: AB6141; UID:21016719; PMID:11130712

A/Accession: B96722

A/Molecule type: DNA

A/Residues: 1-307 <STO>

A/Cross-references: UNIPROT:O04951; UNIPARC:UPT0000130FC4; GB:A/E

C/Genetics:

A/Gene: F20P5.30

A/Map position: 1

C/Superfamily: serine/threonine protein phosphatase: phosphoeste-

C/Keywords: iron; metalloprotein; phosphoric monoester hydrolase

F;21-180/Domain: phosphoprotein phosphatase homology <PPP>

F;49-117/Domain: phosphoesterase core homology <PEC>

F;55,57,83/Binding site: Iron (Asp, His, Asp) #status predicted

F;83,115,165,239/Binding site: zinc (Asp, Asn, His, His) #status

F;86,116,263/Active site: Asp, His, Tyr #status predicted

F;87,212/binding site: substrate phosphate (Arg) #status predict-

```
Query Match          89.5%; Score 1495; DB 1; Length 307  
Best Local Similarity 87.9%; Pred. No. 1.4e-125;  
Matches 268; Conservative 23; Mismatches 14; Indels
```

QY 2 PSYADVDRQIEQLSECKPLSELVKNLCDQAARTILVEEWNVPVKCPVT
| | | : | | | : | | | : | | | : | | | : | | |
Db 3 PATGDSDRQIEQLMECKALSETVMKLCEHAKTILLVEEYNVPVKCPVT
| | | : | | | : | | | : | | | : | | | : | | |

QY 62 LIELFRIGGKAPDTNYLFMGDVVDRGYSVETVSLIALVKVRDRDRIITLI

Db 63 LIELFRIGGSDPTNYLFMGDYVDRGYYSVETVSLVALLVKVRYDRITILRGNHESRQIT 122
Qy 122 QVGYFYDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTHIRALD 181
Db 123 QVGYFYDECLRYKGNANWKYFTDLFDYLPALTALIEHVSQVCLHGLSPSLDTHIRSLD 182
Qy 182 RIQVPEHGPMDLLWSDDRCRGGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLV 241
Db 183 RIQVPEHGPMDLLWSDDRCRGGISPRGAGYTFGQDIATQFNHTNGLSLISRAHQLV 242
Qy 242 MEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETNRSFLOPEAPRQSEPDVTRKT 301
Db 243 MEGFNWQCKNVVTVFSPAPNYCYRCGNMAAILEIGENMDQNFLOPDAPRQVEPETTRKT 302
Qy 302 PDYFL 306
Db 303 PDYFL 307

RESULT 5
T03389
probable phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03389
R/Chang, M.C.; Chen, X.; Wang, B.
submitted to the EMBL Data Library, February 1996
A/Reference number: Z14920
A/Accession: T03389
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-306 <CHA>
A/Cross-references: UNIPROT:Q42981; UNIPARC:UPI00000A2648; EMBL:U49113; NID:G1218053; PI
A/Experimental source: seed, strain IR36
C/Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosph
C/Keywords: phosphoric monoester hydrolase
F:20-279/Domain: phosphoprotein phosphatase homology <PPP>
F:48-116/Domain: phosphoesterase core homology <PEC>

Query Match 88.7%; Score 1481; DB 2; Length 306;
Best Local Similarity 86.3%; Pred. No. 2.4e-124;
Matches 264; Conservative 27; Mismatches 15; Indels 0; Gaps 0;
Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEMNVQPKCPVTTCGDIHQGFH 60
Db 1 MPSHADLRQISLRECKPLSEVKNLCEQAKAILMEEMNVQPKCPVTTCGDIHQGFH 60
Qy 61 DLIELFRIGGKAPDNTNYLFMGDYVDRGYYSVETVSLVALLVKVRYDRITILRGNHESRQI 120
Db 61 DLIELFRIGGSDPTNYLFMGDYVDRGYYSVETVLLVALLVKVRYERITILRGNHESRQI 120
Qy 121 TVQVGYFDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTHIRAL 180
Db 121 TVQVGYFDECLRYKGNANWKYFADLFDYLPALTALVENQVCLHGLSPSLDTHIRAL 180
Qy 181 DRIQVPEHGPMDLLWSDDRCRGGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240
Db 181 DRIQVPEHGPMDLLWSDDRCRGGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL 240
Qy 241 VMEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETNRSFLOPEAPRQSEPDVTRK 300
Db 241 VMEGYNWQDKNVVTVFSPAPNYCYRCGNMAAILEIGENMDQNFLOPDAPRQIDPDTRK 300
Qy 301 TPDYFL 306
Db 301 TPDYFL 306

RESULT 6
T03599
phosphoprotein phosphatase (EC 3.1.3.16) 2A, npp4 - common tobacco
C/Species: Nicotiana tabacum (common tobacco)

C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
C/Accession: T03599
R/Suh, M.; Cho, H.; Kim, Y.; Liu, J.; Lee, H.
Plant Mol. Biol. 36, 315-322, 1998
A/Title: Multiple genes encoding serine/threonine protein phosphat
A/Reference number: Z14967; MUID:98145437; PMID:9484443
A/Accession: T03599
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-302 <SUH>
A/Cross-references: UNIPROT:O04859; UNIPARC:UPI00000A0317; EMBL:
A/Experimental source: cultivar Xanth
C/Genetics:
A/Gene: npp4
C/Superfamily: serine/threonine protein phosphatase; phosphoeste
C/Keywords: iron; phosphoric monoester hydrolase; serine/threoni
F:18-275/Domain: phosphoprotein phosphatase homology <PPP>
F:44-112/Domain: phosphoesterase core homology <PEC>

Query Match 86.5%; Score 1445; DB 2; Length 302
Best Local Similarity 86.3%; Pred. No. 3.8e-121;
Matches 264; Conservative 17; Mismatches 21; Indels
Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEMNVQPKCPVT 60
Db 1 MPSHG--DRQIAQLMECKPLSEVKNLCDQAGTV--RMNVQPKCPVT 56
Qy 61 DLIELFRIGGKAPDNTNYLFMGDYVDRGYYSVETVSLVALLVKVRYDRITIL 120
Db 57 DLIELFRIGGKAPDNTNYLFMGDYVDRGYYSVETVLLVALLVKVRYDRITIL 116
Qy 121 TVQVGYFDECLRYKGNANWKYFTDLFDYLPALTALIEHEIFCLHGLSPS 180
Db 117 TVQVGYFDECLRYKGNANWKYFTDLFDYLPALTALIESQIFCLHGLSPS 176
Qy 181 DRIQVPEHGPMDLLWSDDRCRGGISPRGAGYTFGQDIAEQFNHTN 240
Db 177 DRIQVPEHGPMDLLWSDDRCRGGISPRGAGYTFGQDIAEQFNHTN 236
Qy 241 VMEGYNWQDKNVVTVFSPAPNYCYRCGNMAAIMEIDETNRSFLOPEAP 300
Db 237 VMDGNWQDKNVVTVFSPAPNYCYRCGNMAAILEIGENLQNFLOPDAP 296
Qy 301 TPDYFL 306
Db 297 TPDYFL 302

RESULT 7
A27430
phosphoprotein phosphatase (EC 3.1.3.16) 2-alpha catalytic chain
A/Alternate names: phosphoprotein phosphatase 2A-alpha catalytic
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
C/Accession: A27430
R/Stone, S.R.; Hofsteenge, J.; Hemmings, B.A.
Biochemistry 26, 7215-7220, 1987
A/Title: Molecular cloning of cDNAs encoding two isoforms of the
A/Reference number: A27430; MUID:88107662; PMID:2827745
A/Accession: A27430
A/Molecule type: mRNA
A/Residues: 1-309 <STO>
A/Cross-references: UNIPROT:P05323; UNIPARC:UPI0000000C15; GB:M2
C/Superfamily: serine/threonine protein phosphatase; phosphoeste
C/Keywords: iron; metalloprotein; phosphoric monoester hydrolase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His) #status
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predict
Query Match 85.4%; Score 1427; DB 1; Length 305

```

Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

QY 6 DVDROIQLSECKPLSELEVNKLCDQARTILVEEWNVQVKPCVTCGDIHQFHDLIJEL 65
   :::::::::::::::::::::::::::::
Db 9 ELDQWIEQLNECKQLSESVQKSLCEKAKEILTKESNVQEVRCPTVTCGDIHQFHDLMEL 68
   :::::::::::::::::::::::::::::::
QY 66 FRIGKAPDNTNLFMGDYVDGRGYSVETVSLVALVKVRYRDRITILRGNHESRQITQYVG 125
   :::::::::::::::::::::::::::::::
Db 69 FRIGKSPDNTNLFMGDYVDGRGYSVETVTLVALVKVRYRERITILRGNHESRQITQYVG 128
   :::::::::::::::::::::::::::::::
QY 126 FYDECLRYKGNANVWKYFTDLFDYLPALTALIEHEIFCLHGGLSPSLTDLRHLDRIQ 185
   :::::::::::::::::::::::::::::::
Db 129 FYDECLRYKGNANVWKYFTDLFDYLPALTALVDGQIFCLHGGLSPSIDILDRHLDRIQ 188
   :::::::::::::::::::::::::::::::
QY 186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAQLVMEGY 245
   :::::::::::::::::::::::::::::::
Db 189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGLTLVSRHQLVMEGY 248
   :::::::::::::::::::::::::::::::
QY 246 NWCQDNVTVFSAPNYCYRCGNMAAIMEIDTMRSLFQEPAPRQSEPDVTRTPDYF 305
   :::::::::::::::::::::::::::::::
Db 249 NWCHDRNVTVFSAPNYCYRCGNQAAIMELDDTLKYSFLQFDPAPRGPBPHVTRTPDYF 308
   :::::::::::::::::::::::::::::::
QY 306 L 306
   |
Db 309 L 309

RESULT 8
PAHU2A
phosphoprotein phosphatase (EC 3.1.3.16) 2-alpha catalytic chain - human
N:Alternate names: phosphoprotein phosphatase 2A-alpha catalytic chain; protein phosphat
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 05-Oct-2004
C:Accession: S01986; A32143
R:Stone, S.R.; Mayer, R.; Wernet, W.; Maurer, F.; Hofsteenge, J.; Hemmings, B.A.
Nucleic Acids Res. 16, 11365, 1988
A:Title: The nucleotide sequence of the cDNA encoding the human lung protein phosphatase
A:Reference number: S01986; MUID:89083567; PMID:2849764
A:Accession: S01986
A:Molecule type: mRNA
A:Residues: 1-309 <STO>
A:Cross-references: UNIPROT:P05323; UNIPARC:UPI0000000C15; EMBL:X12646; NID:G36119; PIDN
R:Knew-Goodall, Y.; Mayer, R.E.; Maurer, F.; Stone, S.R.; Hemmings, B.A.
Biochemistry 30, 89-97, 1991
A:Title: Structure and transcriptional regulation of protein phosphatase 2A catalytic su
A:Reference number: A37135; MUID:91105105; PMID:1846293
A:Accession: A37135
A:Molecule type: DNA
A:Residues: 1-309 <KHE>
A:Cross-references: UNIPARC:UPI0000000C15; GB:M60483; GB:J05297; NID:G190223; PIDN:AAA36
R:Arino, J.; Woon, C.W.; Brautigan, D.L.; Miller Jr., T.B.; Johnson, G.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 4252-4256, 1988
A:Title: Human liver phosphatase 2A: cDNA and amino acid sequence of two catalytic subun
A:Reference number: A94200; MUID:88248000; PMID:2837763
A:Accession: A32143
A:Molecule type: mRNA
A:Residues: 1-309 <ARI>
A:Cross-references: UNIPARC:UPI0000000C15; GB:J03804; NID:G1707870; PIDN:AAB38019.1; PID
A:Experimental source: liver; clone HL-14
A>Note: the authors translated the codon CAT for residue 63 as Glu
C:Genetics:
A:Gene: GDB:PPP2CA
A:Cross-references: GDB:126878; OMIM:176915
A:Map position: 5q23.2-5q31.2
C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phos
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-speci
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status predicted
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predicted

```

```

Query Match 85.4%; Score 1427; DB 1; Length 309
Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

QY 6 DVDROIQLSECKPLSELEVNKLCDQARTILVEEWNVQVKPCVTCGDIHQFHDLIJEL 3L 65
   :::::::::::::::::::::::::::::::
Db 9 ELDQWIEQLNECKQLSESVQKSLCEKAKEILTKESNVQEVRCPTVTCGDIHQFHDLMEL 3L 68
   :::::::::::::::::::::::::::::::
QY 66 FRIGKAPDNTNLFMGDYVDGRGYSVETVSLVALVKVRYRDRITILRGNHESRQITQYVG 125
   :::::::::::::::::::::::::::::::
Db 69 FRIGKSPDNTNLFMGDYVDGRGYSVETVTLVALVKVRYRERITILRGNHESRQITQYVG 128
   :::::::::::::::::::::::::::::::
QY 126 FYDECLRYKGNANVWKYFTDLFDYLPALTALIEHEIFCLHGGLSPSLTDLRHLDRIQ 3E 185
   :::::::::::::::::::::::::::::::
Db 129 FYDECLRYKGNANVWKYFTDLFDYLPALTALVDGQIFCLHGGLSPSIDILDRHLDRIQ 3E 188
   :::::::::::::::::::::::::::::::
QY 186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAQLVMEGY 3Y 245
   :::::::::::::::::::::::::::::::
Db 189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGLTLVSRHQLVMEGY 3Y 248
   :::::::::::::::::::::::::::::::
QY 246 NWCQDNVTVFSAPNYCYRCGNMAAIMEIDTMRSLFQEPAPRQSEPDVTRTPDYF 3F 305
   :::::::::::::::::::::::::::::::
Db 249 NWCHDRNVTVFSAPNYCYRCGNQAAIMELDDTLKYSFLQFDPAPRGPBPHVTRTPDYF 3F 308
   :::::::::::::::::::::::::::::::
QY 306 L 306
   |
Db 309 L 309

```

```

RESULT 9
PARBAI
phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text_change 0
C:Accession: S00104; S18812; A60240
R:da Cruz e Silva, O.B.; Alenany, S.; Campbell, D.G.; Cohen, P.T.
FEBS Lett. 221, 415-422, 1987
A:Title: Isolation and sequence analysis of a cDNA clone encoding
A:Reference number: S00104; MUID:87304854; PMID:3040474
A:Accession: S00104
A:Molecule type: mRNA
A:Residues: 1-309 <DAC>
A:Cross-references: UNIPROT:P05323; UNIPARC:UPI0000000C15; EMBL:
A:Accession: S18812
A:Molecule type: protein
A:Residues: 9-21;67-80;215-229,'X',231-238;277-298;304-308 <DAC2
A:Cross-references: UNIPARC:UPI00001727FF; UNIPARC:UPI0000172800
R:Stone, S.R.; Hofsteenge, J.; Hemmings, B.A.
Adv. Exp. Med. Biol. 231, 559-566, 1988
A:Title: Primary structure of protein phosphatase 2A as determin
A:Reference number: A60240; MUID:88323941; PMID:2843014
A:Accession: A60240
A:Molecule type: protein
A:Residues: 2-19;26-37;48-62,'X',64-87;137-144;186-190,'X',192-1
A:Cross-references: UNIPARC:UPI0000172804; UNIPARC:UPI0000172805
C:Superfamily: serine/threonine protein phosphatase; phosphoeste
C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase
F:23-282/Domain: phosphoprotein phosphatase homology <PPP>
F:51-119/Domain: phosphoesterase core homology <PEC>
F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted
F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status
F:88,118,265/Active site: Asp, His, Tyr #status predicted
F:89,214/Binding site: substrate phosphate (Arg) #status predict

```

```

Query Match 85.4%; Score 1427; DB 1; Length 309
Best Local Similarity 83.7%; Pred. No. 1.6e-119;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

QY 6 DVDROIQLSECKPLSELEVNKLCDQARTILVEEWNVQVKPCVTCGDIHQFHDLIJEL 3L 65
   :::::::::::::::::::::::::::::::
Db 9 ELDQWIEQLNECKQLSESVQKSLCEKAKEILTKESNVQEVRCPTVTCGDIHQFHDLMEL 3L 68
   :::::::::::::::::::::::::::::::

```

QY	66	FRIGGKAPDNTNLFMGDQVVDGRGYYSVETVSLVALVKVRYRDRITILRGNE	YG 125		
Db	69 <th>FRIGGKSPDNTNLFMGDQVVDGRGYYSVETVTLVALVKVRYRERITILRGNE</th> <th>YG 128</th>	FRIGGKSPDNTNLFMGDQVVDGRGYYSVETVTLVALVKVRYRERITILRGNE	YG 128		
QY	126 <th>FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIEFCLHGGLSPSIDTLI</th> <th>QE 185</th>	FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIEFCLHGGLSPSIDTLI	QE 185		
Db	129 <th>FYDECLRKYGNAVWKYFTDLFDYLPALTALVDGQIFCLHGGLSPSIDTLI</th> <th>QE 188</th>	FYDECLRKYGNAVWKYFTDLFDYLPALTALVDGQIFCLHGGLSPSIDTLI	QE 188		
QY	186 <th>VPHEGPMCDLLWSPDDRCGNGWISPRGAGYTFGQDIAEQFNHTNGLSLVA</th> <th>GY 245</th>	VPHEGPMCDLLWSPDDRCGNGWISPRGAGYTFGQDIAEQFNHTNGLSLVA	GY 245		
Db	189 <th>VPHEGPMCDLLWSPDDRCGNGWISPRGAGYTFGQDISETFNHANGLTIVS</th> <th>GY 248</th>	VPHEGPMCDLLWSPDDRCGNGWISPRGAGYTFGQDISETFNHANGLTIVS	GY 248		
QY	246 <th>NWCODKNVTVFSPAPNTCYRCGNMAAIMEIDTMRSFLQFEPAPRQSEF</th> <th>YF 305</th>	NWCODKNVTVFSPAPNTCYRCGNMAAIMEIDTMRSFLQFEPAPRQSEF	YF 305		
Db	249 <th>NWCHDRNVVTFSPAPNTCYRCGNQAAIMELDDTLKYSLQFDPAPRRGEF</th> <th>YF 308</th>	NWCHDRNVVTFSPAPNTCYRCGNQAAIMELDDTLKYSLQFDPAPRRGEF	YF 308		
QY	306	L 306			
Db	309	L 309			
RESULT 11					
	S10371				
	phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chai				
	C;Species: Bos primigenius taurus (cattle)				
	C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change				
	C;Accession: S10371; S32226				
	R;de Paoli-Roach, A.A.				
	submitted to the EMBL Data Library, March 1990				
	A;Description: Nucleotide sequence of a cDNA encoding the protei				
	A;Reference number: S10371				
	A;Accession: S10371				
	A;Molecule type: mRNA				
	A;Residues: 1-309 <DEP>				
	A;Cross-references: UNIPROT:P05323; UNIPARC:UPI0000000C15; EMBL:				
	A;Experimental source: aortic smooth muscle				
	R;Chen, S.; Boynton, A.				
	submitted to the EMBL Data Library, March 1993				
	A;Description: Nucleotide sequence of a bovine brain cDNA encodi				
	A;Reference number: S32226				
	A;Accession: S32226				
	A;Status: preliminary				
	A;Molecule type: mRNA				
	A;Residues: 1-309 <CHE>				
	A;Cross-references: UNIPARC:UPI0000000C15; EMBL:X72858; NID:g288				
	A;Experimental source: brain				
	C;Superfamily: serine/threonine protein phosphatase; phosphoeste				
	C;Keywords: iron; metalloprotein; phosphoric monoester hydrolase				
	F;23-282/Domain: phosphoprotein phosphatase homology <PPP>				
	F;51-119/Domain: phosphoesterase core homology <PEC>				
	F;57,59,85/Binding site: iron (Asp, His, Asp) #status predicted				
	F;85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status				
	F;88,118,265/Active site: Asp, His, Tyr #status predicted				
	F;89,214/Binding site: substrate phosphate (Arg) #status predict				
Query Match		85.4%; Score 1427; DB 1; Length 309			
Best Local Similarity		83.7%; Pred. No. 1.6e-119;			
Matches 252; Conservative		32; Mismatches 17; Indels			
QY	6	DVDRQTEQLSECKPLSELEVNKLCDOQARTILVEWNVQPVKCPVTVCGD1	EL 65		
Db	9	ELDQWTEQLNECKQLSESVKSLCEKAKEILTKESENQVEVRCPVTVCGDV	EL 68		
QY	66 <th>FRIGGKAPDNTNLFMGDQVVDGRGYYSVETVSLVALVKVRYRDRITILRGNE</th> <td>YG 125</td>	FRIGGKAPDNTNLFMGDQVVDGRGYYSVETVSLVALVKVRYRDRITILRGNE	YG 125		
Db	69 <th>FRIGGKSPDNTNLFMGDQVVDGRGYYSVETVTLVALVKVRYRERITILRGNE</th> <td>YG 128</td>	FRIGGKSPDNTNLFMGDQVVDGRGYYSVETVTLVALVKVRYRERITILRGNE	YG 128		
QY	126 <th>FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIEFCLHGGLSPSIDTLI</th> <td>QE 185</td>	FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIEFCLHGGLSPSIDTLI	QE 185		
Db	129 <th>FYDECLRKYGNAVWKYFTDLFDYLPALTALVDGQIFCLHGGLSPSIDTLI</th> <td>QE 188</td>	FYDECLRKYGNAVWKYFTDLFDYLPALTALVDGQIFCLHGGLSPSIDTLI	QE 188		
QY	186 <th>VPHEGPMCDLLWSPDDRCGNGWISPRGAGYTFGQDIAEQFNHTNGLSLVA</th> <td>GY 245</td>	VPHEGPMCDLLWSPDDRCGNGWISPRGAGYTFGQDIAEQFNHTNGLSLVA	GY 245		

Db 189 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDISETFNHANGTLVSRHQVLVMEGY 248

QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEPDVTRKTPDYF 305

Db 249 NWCHDRNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEPDVTRKTPDYF 308

QY 306 L 306

Db 309 L 309

RESULT 12

S20348

phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain - clawed frog

C:Species: Xenopus sp. (clawed frog)

C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004

C:Accession: S20348

R:Cormier, P.; Osborne, H.B.; Bassez, T.; Poulhe, R.; Mulner-Lorillon, O.

FEBS Lett. 295, 185-188, 1991

A>Title: Protein phosphatase 2(A) from Xenopus oocytes. Characterization during meiotic

A:Reference number: S20348; MUID:92111736; PMID:1662645

A:Accession: S20348

A:Molecule type: mRNA

A:Residues: 1-309 <COR>

A:Cross-references: UNIPARC:UPI00000FE513; EMBL:X62114

C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phospho

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specif

F:23-282/Domain: phosphoprotein phosphatase homology <PPP>

F:51-119/Domain: phosphoesterase core homology <PEC>

F:57-59.85/Binding site: iron (Asp, His, Asp) #status predicted

F:85.117,167,241/Binding site: zinc (Asp, Asn, His, His) #status predicted

F:88.118,265/Active site: Asp, His, Tyr #status predicted

F:89.214/Binding site: substrate phosphate (Arg) #status predicted

Query Match 85.1%; Score 1421; DB 1; Length 309;

Best Local Similarity 83.4%; Pred. No. 5.4e-119;

Matches 251; Conservative 32; Mismatches 18; Indels 0; Gaps 0;

QY 6 DVDRIEQLSECKPLSELEVNKLCDOARTILVEEWNVQPKVTCGDIHQFDLIEL 65

Db 9 ELDEWIEQLNECKQLTEGQVSLCEKAKEILTKESNVQEVCPVTCGVDVHQFDHLMEL 68

QY 66 FRIGKAPDNTYLFMGDYVDRGYYSVETVSLVVALVKVRYRDRITILRGHESRQITQVYG 125

Db 69 FRIGGKSPDNTYLFMGDYVDRGYYSVETVTLVVALVKVRYRERITILRGHESRQITQVYG 128

QY 126 FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSLPSLDLDRIOE 185

Db 129 FYDECLRKYGNAVWKYFTDLFDYLPALTALVQGIQFCLHGGSLPSLDLDRIOE 188

QY 186 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARHQLVMEGY 245

Db 189 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDISETFNHANGTLVSRHQVLVMEGY 248

QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEPDVTRKTPDYF 305

Db 249 NWCHDRNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEPDVTRKTPDYF 308

QY 306 L 306

Db 309 L 309

RESULT 13

S12961

phosphoprotein phosphatase (EC 3.1.3.16) 2A-28D catalytic chain - fruit fly (Drosophila

C:Species: Drosophila melanogaster

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004

C:Accession: S12961

R:Orgad, S.; Brewis, N.D.; Alphey, L.; Axton, J.M.; Dudai, Y.; Cohen, P.T.W.

FEBS Lett. 275, 44-48, 1990

A>Title: The structure of protein phosphatase 2A is as highly conserved as that of prote

A:Reference number: S12961; MUID:91085575; PMID:2175718

A:Accession: S12961

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-309 <ORG>

A:Cross-references: UNIPROT:P23696; UNIPARC:UPI0000007461; GB:X5;

C:Genetics;

A:Gene: FlyBase:Pp2A-28D

A:Cross-references: FlyBase:FBgn0004177

A:Map position: 2L 28D2-4

C:Superfamily: serine/threonine protein phosphatase; phosphoeste

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase

F:23-282/Domain: phosphoprotein phosphatase homology <PPP>

F:51-119/Domain: phosphoesterase core homology <PEC>

F:57.59.85/Binding site: iron (Asp, His, Asp) #status predicted

F:85.117,167,241/Binding site: zinc (Asp, Asn, His, His) #status

F:88.118,265/Active site: Asp, His, Tyr #status predicted

F:89.214/Binding site: substrate phosphate (Arg) #status predict

Query Match 84.6%; Score 1412; DB 1; Length 309

Best Local Similarity 82.7%; Pred. No. 3.5e-118;

Matches 249; Conservative 34; Mismatches 18; Indels

QY 6 DVDRIEQLSECKPLSELEVNKLCDOARTILVEEWNVQPKVTCGDIHQFDLIEL 65

Db 9 ELDEWIEQLNECKQLTEGQVSLCEKAKEILTKESNVQEVCPVTCGVDV 68

QY 66 FRIGKAPDNTYLFMGDYVDRGYYSVETVSLVVALVKVRYRDRITILRGH 125

Db 69 FRIGGKSPDNTYLFMGDYVDRGYYSVETVTLVVALVKVRYRERITILRGH 128

QY 126 FYDECLRKYGNAVWKYFTDLFDYLPALTALIEHEIFCLHGGSLPSLDL 185

Db 129 FYDECLRKYGNAVWKYFTDLFDYLPALTALVQGIQFCLHGGSLPSLDL 188

QY 186 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVA 245

Db 189 VPHEGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDISETFNHTNGLTIVS 248

QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEPD 305

Db 249 NWCHDRNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPRQSEPD 308

QY 306 L 306

Db 309 L 309

RESULT 14

PAHU2B

phosphoprotein phosphatase (EC 3.1.3.16) 2-beta catalytic chain

N:Alternate names: protein phosphatase 2A-beta isoform catalytic

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change

C:Accession: B37135; S01985; B32143; S09378; A34060

R:Khaw-Goodall, Y.; Mayer, R.E.; Maurer, F.; Stone, S.R.; Hemmin

Biochemistry 30, 89-97, 1991

A>Title: Structure and transcriptional regulation of protein pho

A:Reference number: A37135; MUID:91105105; PMID:1846293

A:Accession: B37135

A:Molecule type: DNA

A:Residues: 1-309 <KHE>

A:Cross-references: UNIPROT:P11082; UNIPARC:UPI00000000CC2; GB:M6

R:Hemmings, B.A.; Wernet, W.; Mayer, R.; Maurer, F.; Hofsteenge,

Nucleic Acids Res. 16, 11366, 1988

A>Title: The nucleotide sequence of the cDNA encoding the human

A:Reference number: S01985; MUID:89083568; PMID:2849765

A:Accession: S01985

A:Molecule type: mRNA

A:Residues: 1-309 <KHE>

A:Cross-references: UNIPARC:UPI00000000CC2; EMBL:X12656; NID:9355;

R:Arino, J.; Woon, C.W.; Brautigan, D.L.; Miller Jr., T.B.; John

Proc. Natl. Acad. Sci. U.S.A. 85, 4252-4256, 1988

A>Title: Human liver phosphatase 2A: cDNA and amino acid sequenc

A:Reference number: A94200; MUID:88248000; PMID:2837763

A:Accession: B32143

A:Molecule type: mRNA

A:Residues: 2-18, D', 20-309 <AR2>

A:Cross-references: UNIPARC:UPI000016A537; GB:J03805; NID:gl78437; PIDN:AAB38020.1; PID:

A:Experimental source: liver; clone HL-1

A>Note: the authors translated the codon GAC for residue 18 as Glu

R;Virshup, D.M.; Kauffman, M.G.; Kelly, T.J.

EMBO J. 8, 3891-3898, 1989

A:Title: Activation of SV40 DNA replication in vitro by cellular protein phosphatase 2A.

A:Reference number: S09378; MUID:90059993; PMID:2555176

A:Accession: S09378

A:Molecule type: protein

A:Residues: 91-97;111-114;122-127;137-144;207-238 <VIR>

A:Cross-references: UNIPARC:UPI0000172807; UNIPARC:UPI000017280C; UNIPARC:UPI000017280D;

R;Pallas, D.C.; Shahrak, L.K.; Martin, B.L.; Jaspers, S.; Miller, T.B.; Brautigan, D.L.;

Cell 60, 167-176, 1990

A:Title: Polyoma small and middle T antigens and SV40 small t antigen form stable complex

A:Reference number: A34060; MUID:90106638; PMID:2153055

A:Accession: A34060

A:Molecule type: protein

A:Residues: 75-89;215-234;X', 270-294;303-309 <PAL>

A:Cross-references: UNIPARC:UPI0000172810; UNIPARC:UPI0000172811; UNIPARC:UPI0000172812;

C:Genetics: GDB:PPP2CB

A:Gene: GDB:PPP2CB

A:Cross-references: GDB:126879; OMIM:176916

A:Map position: 8p12-8p11.2

C:Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phospho

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-specif

F:23-282/Domain: phosphoprotein phosphatase homology <PPP>

F:51-119/Domain: phosphoesterase core homology <PEC>

F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted

F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #status predicted

F:88,118,265/Active site: Asp, His, Tyr #status predicted

F:89,214/Binding site: substrate phosphate (Arg) #status predicted

Query Match 84.5%; Score 1411; DB 1; Length 309;

Best Local Similarity 82.4%; Pred. No. 4.2e-118;

Matches 248; Conservative 34; Mismatches 19; Indels 0; Gaps 0;

QY 6 DVDRIQLSECKPLSELEVNKLCDOARTILVEENWQVVKCPVTVCGDI 65

DB 9 ELDQWVEQLNECKQLNENQVRLCEKAEILTKESNVQEVRCFVTVCGDV 68

QY 66 FRIGGKAPDTNLYFMGDYVDRGYYSVETVLLVALVKVRYDRITILRGNE 125

DB 69 FRIGGKSPDTNLYFMGDYVDRGYYSVETVLLVALVKVRYPERITILRGNE 128

QY 126 FYDECLRKYGNNVWKYFTDLFDYLPALTALIEHEIFCLHGGSLPSLDRIOE 185

DB 129 FYDECLRKYGNNVWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDTLDRALDRIOE 188

QY 186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLVMGY 245

DB 189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGITLVSRAHQLVMGY 248

QY 246 NWCQDKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPRQSEPDVTRKTPDYF 305

DB 249 NWCQDKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPRQSEPDVTRKTPDYF 308

QY 306 L 306

DB 309 L 309

RESULT 15

PARB2B

phosphoprotein phosphatase (EC 3.1.3.16) 2A-beta catalytic chain - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004

C:Accession: S00220

R:da Cruz e Silva, O.B.; Cohen, P.T.W.

FEBS Lett. 226, 176-178, 1987

A:Title: A second catalytic subunit of type-2A protein phosphatase

A:Reference number: S00220; MUID:88083628; PMID:2826253

A:Accession: S00220

A:Molecule type: mRNA

A:Residues: 1-309 <DA1>

A:Cross-references: UNIPROT:P11611; UNIPARC:UPI0000130FC8; EMBL:

C:Superfamily: serine/threonine protein phosphatase; phosphoeste

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase

F:23-282/Domain: phosphoprotein phosphatase homology <PPP>

F:51-119/Domain: phosphoesterase core homology <PEC>

F:57,59,85/Binding site: iron (Asp, His, Asp) #status predicted

F:85,117,167,241/Binding site: zinc (Asp, Asn, His, His) #statue

F:88,118,265/Active site: Asp, His, Tyr #status predicted

F:89,214/Binding site: substrate phosphate (Arg) #status predict

Query Match 84.5%; Score 1411; DB 1; Length 309

Best Local Similarity 82.4%; Pred. No. 4.2e-118;

Matches 248; Conservative 34; Mismatches 19; Indels

QY 6 DVDRIQLSECKPLSELEVNKLCDOARTILVEENWQVVKCPVTVCGDI 65

DB 9 ELDQWVEQLNECKQLNENQVRLCEKAEILTKESNVQEVRCFVTVCGDV 68

QY 66 FRIGGKAPDTNLYFMGDYVDRGYYSVETVLLVALVKVRYDRITILRGNE 125

DB 69 FRIGGKSPDTNLYFMGDYVDRGYYSVETVLLVALVKVRYPERITILRGNE 128

QY 126 FYDECLRKYGNNVWKYFTDLFDYLPALTALIEHEIFCLHGGSLPSLDTLL 185

DB 129 FYDECLRKYGNNVWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSIDTL 188

QY 186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVA 245

DB 189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGITLVS 248

QY 246 NWCQDKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPRQSEF 305

DB 249 NWCQDKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQEPAPRQSEF 308

QY 306 L 306

DB 309 L 309

Search completed: December 9, 2005, 10:24:08

Job time : 41 secs

rabbit skeletal n

NID:gl684; PIDN:C
e homology; phosph
/threonine-specif

ed

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2005, 10:13:51 ; Search time 46 Seconds
(without alignments)
549.973 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MPSVADVDRIEQLSECKPL.....EPAPRQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5-COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6-COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H-COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1670	100.0	306	2	US-09-828-302-13
2	1427	85.4	309	2	US-09-538-092-854
3	1427	85.4	355	2	US-09-949-016-11414
4	1411	84.5	309	2	US-09-538-092-902
5	1411	84.5	309	2	US-09-949-016-6461
6	1411	84.5	311	2	US-09-949-016-11335
7	1326	79.4	325	2	US-09-190-976B-10
8	1291	77.3	377	2	US-09-487-558B-270
9	1286	77.0	369	2	US-09-487-558B-268
10	1137.5	68.1	341	2	US-09-949-016-8780
11	973	58.3	312	2	US-09-949-016-9733
12	963.5	57.7	318	2	US-09-248-796A-18310
13	942.5	56.4	303	2	US-09-916-338A-2
14	786	47.1	271	2	US-09-248-796A-18309
15	757	45.3	323	2	US-09-538-092-1093
16	756	45.3	312	2	US-09-538-092-256
17	739	44.3	330	2	US-09-167-206-6
18	739	44.3	330	2	US-09-538-092-873
19	739	44.3	374	2	US-09-949-016-7363
20	736	44.1	327	2	US-09-538-092-1095
21	736	44.1	327	2	US-09-949-016-6266
22	736	44.1	356	2	US-09-949-016-8084
23	731	43.8	330	2	US-09-190-976B-8
24	729.5	43.7	319	2	US-09-248-796A-18323
25	696.5	41.7	260	2	US-09-248-796A-18344
26	639	38.3	184	2	US-09-248-796A-18313
27	629.5	37.7	692	2	US-09-487-558B-274

28	614.5	36.8	710	2	US-09-487-558B-276	Sequ
29	565	33.8	502	2	US-09-949-016-10218	18, A
30	565	33.8	510	2	US-09-744-016A-6	Appli
31	565	33.8	521	2	US-09-538-092-1283	3, Ap
32	565	33.8	523	2	US-09-744-016A-21	Appli
33	565	33.8	533	2	US-09-744-016A-18	Appli
34	559	33.5	487	1	US-08-452-722-7	Sequ
35	559	33.5	487	1	US-08-404-731A-7	Appli
36	559	33.5	487	1	US-08-344-227-7	Appli
37	559	33.5	487	1	US-08-503-226B-7	Appli
38	559	33.5	487	2	US-08-721-458B-7	Appli
39	559	33.5	528	2	US-09-744-016A-9	Appli
40	559	33.5	530	2	US-09-949-016-11683	83, A
41	559	33.5	535	2	US-09-744-016A-24	Appli
42	543	32.5	499	2	US-09-949-016-7370	0, Ap
43	540	32.3	553	2	US-09-744-016A-27	Appli
44	539.5	32.3	502	2	US-09-949-016-6642	2, Ap
45	539.5	32.3	509	2	US-09-744-016A-12	Appli

ALIGNMENTS

RESULT 1

US-09-828-302-13

; Sequence 13, Application US/09828302

; Patent No. 6818805

; GENERAL INFORMATION:

; APPLICANT: COSTA E SILVA, OSWALDO DA

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: CHEN, ROUYING

; APPLICANT: ISHITANI, MANABU

; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND V

; FILE REFERENCE: 16313-0029

; CURRENT APPLICATION NUMBER: US/09/828,302

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/196,001

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 13

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Physcomitrella patens

US-09-828-302-13

Query Match	100.0%	Score 1670;	DB 2;	Length 30
Best Local Similarity	100.0%	Pred. No. 1.9e-178;		
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Qy	1	MPSVADVDRIEQLSECKPLSELEVNKLCQARTILVEENNVQPKCPVT		1FH 60
Db	1	MPSVADVDRIEQLSECKPLSELEVNKLCQARTILVEENNVQPKCPVT		1FH 60
Qy	61	DLIELFRIGGKAPNTNLFMGDDYDRGYYSVETVSLVALKVRVDRITTI		QI 120
Db	61	DLIELFRIGGKAPNTNLFMGDDYDRGYYSVETVSLVALKVRVDRITTI		QI 120
Qy	121	TQVYGFYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGGGLSPS		AL 180
Db	121	TQVYGFYDECLRKYGNNVWKYFTDLFDYLPALTALIEHIFCLHGGGLSPS		AL 180
Qy	181	DRIVEPHEGPMCDLLMSDDPDRCGWGISPRGAGYTFQODIAEQFNHTNG		QL 240
Db	181	DRIVEPHEGPMCDLLMSDDPDRCGWGISPRGAGYTFQODIAEQFNHTNG		QL 240
Qy	241	VMGYNNCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAF		RK 300
Db	241	VMGYNNCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAF		RK 300
Qy	301	TPDYFL 306		

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Db          301 TPDYFL 306

RESULT 2
US-09-538-092-854
; Sequence 854, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 854
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P05323
US-09-538-092-854

Query Match      85.4%; Score 1427; DB 2; Length 309;
Best Local Similarity 83.7%; Pred. No. 3.3e-151;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

Qy      6 DVDRIEQLSECKPLSELEVNKLCDOARTILVBEWNVQPVKCPVTCGDHLLIEL 65
      :::::::::::::::::::::
Db      9 ELDQWIEQLNECKQLSESVKSLCEKAKEILTKESNVQEVRCPTVCGDVGQFHDLMEL 68
      :::::::::::::::::::::

Qy      66 FRIGKAPDPTNYLFMGDYVDRGYYSVETVSLVALLVKVRYRDRITILRGNSHQITQVYG 125
      :::::::::::::::::::::
Db      69 FRIGKSPDPTNYLFMGDYVDRGYYSVETVTLVALLVKVRYRDRITILRGNSHQITQVYG 128
      :::::::::::::::::::::

Qy      126 FYDECLRKYGNANWKYFTDLFDYLPALTALTEHEIFCLHGLSPSLDTHIRALDRLOE 185
      :::::::::::::::::::::
Db      129 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGLSPSIDTLDHIRALDRLOE 188
      :::::::::::::::::::::

Qy      186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLVMEGY 245
      :::::::::::::::::::::
Db      189 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGTLVLSRAHQLVMEGY 248
      :::::::::::::::::::::

Qy      246 NWCODKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
      :::::::::::::::::::::
Db      249 NWCHDRNVTVFSAFNPCYRCGNQAAIMEIDDTLKYSLQFDPAPRGPETHVTRTPDYF 308
      :::::::::::::::::::::

Qy      306 L 306
      |
Db      309 L 309

RESULT 3
US-09-949-016-11414
; Sequence 11414, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11414
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11414

Query Match      85.4%; Score 1427; DB 2; Length 355
Best Local Similarity 83.7%; Pred. No. 4.1e-151;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

Qy      6 DVDRIEQLSECKPLSELEVNKLCDOARTILVBEWNVQPVKCPVTCGDHII 65
      :::::::::::::::::::::
Db      55 ELDQWIEQLNECKQLSESVKSLCEKAKEILTKESNVQEVRCPTVTCGDV 114
      :::::::::::::::::::::

Qy      66 FRIGKAPDPTNYLFMGDYVDRGYYSVETVSLVALLVKVRYRDRITILRGNH 125
      :::::::::::::::::::::
Db      115 FRIGKSPDPTNYLFMGDYVDRGYYSVETVTLVALLVKVRYRDRITILRGNH 174
      :::::::::::::::::::::

Qy      126 FYDECLRKYGNANWKYFTDLFDYLPALTALTEHEIFCLHGLSPSLDTHLDI 185
      :::::::::::::::::::::
Db      175 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGLSPSIDTLDI 234
      :::::::::::::::::::::

Qy      186 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSLVAI 245
      :::::::::::::::::::::
Db      235 VPHEGPMCDLLWSDPDDRCGWSISPRGAGYTFGQDISETFNHANGTLVLSI 294
      :::::::::::::::::::::

Qy      246 NWCODKNVTVFSAFNPCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPI 305
      :::::::::::::::::::::
Db      295 NWCHDRNVTVFSAFNPCYRCGNQAAIMEIDDTLKYSLQFDPAPRGEPI 354
      :::::::::::::::::::::

Qy      306 L 306
      |
Db      355 L 355

RESULT 4
US-09-538-092-902
; Sequence 902, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of U
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 902
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P11082
US-09-538-092-902

Query Match      84.5%; Score 1411; DB 2; Length 309
Best Local Similarity 82.4%; Pred. No. 2e-149;
Matches 248; Conservative 34; Mismatches 19; Indels 0;

Qy      6 DVDRIEQLSECKPLSELEVNKLCDOARTILVBEWNVQPVKCPVTCGDHII 65
      :::::::::::::::::::::
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Db 9 ELDQWVEQLNECKQLNENQVRLCEKAKEILLTKESNVQEVRCPTVCGDVHGQFHDLMEL 68
QY 66 FRIGKAPDNTNLFMGDYYDRGYYSVETVLLVALKVRYDRITILRGHESRQITQYVG 125
Db 69 FRIGKSPDNTNLFMGDYYDRGYYSVETVLLVALKVRYPERITILRGHESRQITQYVG 128
QY 126 FYDECLRKYGNANWKYFTDLFDYLPALTALIEHEIFCLHGGLSPLSLDTHIRALDRIOE 185
Db 129 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGGLSPLSLDTHIRALDRIOE 188
QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLWMEGY 245
Db 189 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNANGLTLSRAHQLWMEGY 248
QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
Db 249 NWCHDRNVTVFSAPNYCYRCGNMAAIMEIDETLTKYSLQFDPAPRGPETHVTRTPDYF 308
QY 306 L 306
Db 309 L 309
RESULT 5
US-09-949-016-6461
; Sequence 6461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6461
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6461
Query Match 84.5%; Score 1411; DB 2; Length 309;
Best Local Similarity 82.4%; Pred. No. 2e-149;
Matches 248; Conservative 34; Mismatches 19; Indels 0; Gaps 0;
QY 6 DVDRIQEIQLSECKPLSELEVNLCDOARTILVEENNVQVPCVTVCGDIHQFHDLMEL 65
Db 9 ELDQWVEQLNECKQLNENQVRLCEKAKEILLTKESNVQEVRCPTVCGDVHGQFHDLMEL 68
QY 66 FRIGKAPDNTNLFMGDYYDRGYYSVETVLLVALKVRYDRITILRGHESRQITQYVG 125
Db 69 FRIGKSPDNTNLFMGDYYDRGYYSVETVLLVALKVRYPERITILRGHESRQITQYVG 128
QY 126 FYDECLRKYGNANWKYFTDLFDYLPALTALIEHEIFCLHGGLSPLSLDTHIRALDRIOE 185
Db 129 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGGLSPLSLDTHIRALDRIOE 188
QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQLWMEGY 245
Db 189 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNANGLTLSRAHQLWMEGY 248
QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPDVTRKTPDYF 305
Db 249 NWCHDRNVTVFSAPNYCYRCGNMAAIMEIDETLTKYSLQFDPAPRGPETHVTRTPDYF 308
QY 306 L 306

Db 309 L 309
RESULT 6
US-09-949-016-11335
; Sequence 11335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11335
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11335
Query Match 84.5%; Score 1411; DB 2; Length 311
Best Local Similarity 82.4%; Pred. No. 2.1e-149;
Matches 248; Conservative 34; Mismatches 19; Indels 0;
QY 6 DVDRIQEIQLSECKPLSELEVNLCDOARTILVEENNVQVPCVTVCGDI 65
Db 11 ELDQWVEQLNECKQLNENQVRLCEKAKEILLTKESNVQEVRCPTVCGDV 70
QY 66 FRIGKAPDNTNLFMGDYYDRGYYSVETVLLVALKVRYDRITILRGH 125
Db 71 FRIGKSPDNTNLFMGDYYDRGYYSVETVLLVALKVRYPERITILRGH 130
QY 126 FYDECLRKYGNANWKYFTDLFDYLPALTALIEHEIFCLHGGLSPLSLD 185
Db 131 FYDECLRKYGNANWKYFTDLFDYLPALTALVDCQIFCLHGGLSPLSLD 190
QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSL 245
Db 191 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNANGLT 250
QY 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSE 305
Db 251 NWCHDRNVTVFSAPNYCYRCGNMAAIMEIDETLTKYSLQFDPAPRGE 310
QY 306 L 306
Db 311 L 311
RESULT 7
US-09-190-976B-10
; Sequence 10, Application US/09190976B
; Patent No. 6815187
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael
; Horowitz, Arie
; TITLE OF INVENTION: Stimulation of angiogenesis via
; syndecan-4 cytoplasmic domain signa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David Frashker, Esq.
; STREET: P.O. Box 5387
; CITY: Magnolia
; STATE: Massachusetts
; highway

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; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 270
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-270

Query Match 77.3%; Score 1291; DB 2; Length 377
Best Local Similarity 76.3%; Pred. No. 7.9e-136;
Matches 229; Conservative 34; Mismatches 37; Indels

QY 7 VDRQIEQLSECKPLSELEVKNLCDQARTILVEEMNVQPVKCPVTWCGDIH(
Db 78 LDQWIEHLKCEPLSEDDVARLCKMAVDVLOPEENVKPINVPVITICGDVH(
QY 67 RIGGKAPDNTYLFMGDYYVDRGVSVETVSLILVALKVRDRITILRGNH(
Db 138 KIGGCPDNTYLFMGDYYVDRGVSVETVSYLVAMKVRPHRITILRGNH(
QY 127 YDECLRKTYGNANVWYFTDLFDYLPALTALIBIEIFCLHGGGLSPSLDTLDH
Db 198 YDECLRKYSANVWKMTDLFDYFPVTALVDNKIFCLHGGGLSPMIETIDQ
QY 187 PHEGPMCDLLWSDDPRDCGWSIGSPRGAGYTFGQDTAQENHTNGLSLVAR(
Db 258 PHEGPMCDLLWSDDPRDCGWSIGSPRGAGFTGQDISEQFNHTNDSLAR(
QY 247 WCQDNVWTFVSAPNVCYRCGNMAAIMEIDETMNSRFQFEPAPRQSEPD'
Db 318 WSHQNVVTFISAPNVCYRCGNQAAMEVDENHNRFQLOYDPSVRGPEPT'

RESULT 9
US-09-487-558B-268
; Sequence 268, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolit-
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 268
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-268

Query Match 77.0%; Score 1286; DB 2; Length 369
Best Local Similarity 75.7%; Pred. No. 2.8e-135;
Matches 227; Conservative 35; Mismatches 37; Indels

QY 7 VDRQIEQLSECKPLSELEVKNLCDQARTILVEEMNVQPVKCPVTWCGDIH(

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Db 70 LDQWIEHLSKCEPLSEDDVARLCKMAVDVLQFEENVKPINVPVTICGDVHGQFHDLLLELF 129
Qy 67 RIGGKAPDNTNLFMGDYVDGRGYVSVETVSLVVALKVYRDRDITILRGHSHESQITQVYGF 126
Db 130 KIGGCPDNTNLFMGDYVDGRGYVSVETVSLVVALKVYRDRDITILRGHSHESQITQVYGF 189
Qy 127 YDECLRKYGANVWKFYDLPDLYPLTALIEHIEFCLHGLSPSLDTHIRALDRIOEV 186
Db 190 YDECLRKYGANVWKFYDLPDLYPLTALIEHIEFCLHGLSPSLDTHIRALDRIOEV 249
Qy 187 PHEGPMCDLLWSDDPDRCGWGISPRGAGYTFQODTAEQNFHTNGLSVARAHQVMEGYN 246
Db 250 PHEGPMCDLLWSDDPDRCGWGISPRGAGYTFQODTAEQNFHTNGLSVARAHQVMEGYN 309
Qy 247 WQODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPQSEPDVTRKTPDYFL 306
Db 310 WSHQNVVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPQSEPDVTRKTPDYFL 369

RESULT 10
US-09-949-016-8780
; Sequence 8780, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8780
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8780
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Query Match 68.1%; Score 1137.5; DB 2; Length 341;
Best Local Similarity 66.4%; Pred. No. 1.1e-118;
Matches 204; Conservative 46; Mismatches 56; Indels 1; Gaps 1;

Qy 1 MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENWVQVKCPVTVCDDIHGQFH 60
Db 35 MAEISDLDRQIEQLSECKPLSELEVKNLCDQARTILVEENWVQVKCPVTVCDDIHGQFY 94
Qy 61 DLIELFRIGKAPDNTNLFMGDYVDGRGYVSVETVSLVVALKVYRDRDITILRGHSHESQI 120
Db 95 DLKELFRVGGDVPETNLFMGDYVDGRGYVSVETVSLVVALKVYRDRDITILRGHSHESQI 154
Qy 121 TVQVGFYDECLRKYGANVWKFYDLPDLYPLTALIEHIEFCLHGLSPSLDTHIRAL 180
Db 155 TVQVGFYDECLRKYGANVWKFYDLPDLYPLTALIEHIEFCLHGLSPSLDTHIRAL 214
Qy 181 DRIQVPEHGPMDLLWSDDPDRCGWGISPRGAGYTFQODTAEQNFHTNGLSVARAHQV 240
Db 215 DRKQVPEHGPMDLLWSDDPDRCGWGISPRGAGYTFQODTAEQNFHTNGLSVARAHQV 274
Qy 241 VMGYNWQDKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPQSEPDVTRK 300
Db 275 VMGYNWQDKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPQSEPDVTRK 334
Qy 301 -TPDYFL 306
Db 335 PVADYFL 341
```

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RESULT 11
US-09-949-016-9733
; Sequence 9733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9733
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9733

Query Match 58.3%; Score 973; DB 2; Length 312;
Best Local Similarity 58.8%; Pred. No. 2.6e-100;
Matches 177; Conservative 41; Mismatches 83; Indels

Qy 6 DVDRQIEQLSECKPLSELEVKNLCDQARTILVEENWVQVKCPVTVCDDI 65
Db 12 DLKYEIARLCKYLPENDLRLCDYVCDLLEESNVQVSTPTVTCDDI 71
Qy 66 PRIGKAPDNTNLFMGDYVDGRGYVSVETVSLVVALKVYRDRDITILRGH 125
Db 72 FRTGGQVPTNYIFMGDFVDRGYVSVETVSLVVALKVYRDRDITILRGH 131
Qy 126 FYDECLRKYGANVWKFYDLPDLYPLTALIEHIEFCLHGLSPSLDTHI 185
Db 132 FYDECLRKYGANVWKFYDLPDLYPLTALIEHIEFCLHGLSPSLDTHI 191
Qy 186 VPHEGPMCDLLWSDDPDRCGWGISPRGAGYTFQODTAEQNFHTNGLSV 245
Db 192 IPHKGAFCDLVWSDPEDVDVTWAIISPRGAGWLFQAKVTFVHINNKLIC 251
Qy 246 NWCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPQSEF 305
Db 252 KFMFDEKLVTVWSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPQSEF 311
Qy 306 L 306
Db 312 L 312

RESULT 12
US-09-248-796A-18310
; Sequence 18310, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL
; ATED TO THE DIAGNOSIS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18310
; LENGTH: 318
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CANDIDA ALBICANS

; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18310

Query Match 57.7%; Score 963.5; DB 2; Length 318;
Best Local Similarity 56.3%; Pred. No. 3.2e-99;
Matches 175; Conservative 55; Mismatches 66; Indels 15; Gaps 4;

QY 8 DRQIEQLSECKPLSELVKNCDOARTILVEENWVQPKVTVCGDIHQFHDHLELFR 67
DB 11 DOWLEQIKNCISLSSDMKQCELVKELLMEESNIQPVQSVTVCGDIHQFHDHLELFR 70

QY 68 IGGKAP-----DTNYLFMGDYVDRGYYSVETVSLVALVKVRYDRDRTITILRGHSHSQITQV 123
DB 71 TAGGLPSDDNQTNFIFLGDYVDRGYFSLETFTLLMLVKVYKYPHRTITLVRGNHSHSQITQV 130

QY 124 YGFYDECLRKYGNAVWYFTDLPYLPALTALIEHIFCLHGGLSPSLDTHDHRALDRI 183
DB 131 YGFYECLTKYGSTVWYKCCOVDFELAAIDGKILCVHGGLSPEIRMLDQIRVLSRA 190

QY 184 QEVPEHGPCDLLWSDPDRCGWGISPRGAGYTFQODIAEQFNHTNGLSLVARAHQVME 243
DB 191 QEVPEHGPCDLLWSDPDNIDTWAVSPRGAGWLFSGSKVSREPFNHNLIQLIARAHQVME 250

QY 244 GYNW-CQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPRQSEPDVTRKT- 301
DB 251 GFRYHFKEDVVTVWSAPNYCYRCGNVASVMQVDEDFPNFKIFSAV---QDGLSVKNN 307

QY 302 -----PDYFL 306
DB 308 ANKQQRSDYFL 318

RESULT 13
US-09-916-338A-2
; Sequence 2, Application US/09916338A
; Patent No. 6586252
; GENERAL INFORMATION:
; APPLICANT: KANG, JEONG-GU
; APPLICANT: SONG, PILL-SOON
; APPLICANT: PARK, CHUNG-MO
; TITLE OF INVENTION: Nucleic acid molecule encoding the catalytic subunit
; TITLE OF INVENTION: of a Protein Phosphatase 2A that regulates flowering
; TITLE OF INVENTION: time in plants
; FILE REFERENCE: P6690305
; CURRENT APPLICATION NUMBER: US/0916,338A
; CURRENT FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-916-338A-2

Query Match 56.4%; Score 942.5; DB 2; Length 303;
Best Local Similarity 56.3%; Pred. No. 6.6e-97;
Matches 170; Conservative 51; Mismatches 80; Indels 1; Gaps 1;

QY 6 DVDROIOLSECKPLSELVKNCDOARTILVEENWVQPKVTVCGDIHQFHDHLEL 65
DB 2 DUDQWISKVQDQHLEDELQULCEYVKEILLEESNVQVNSPVTVCGDIHQFHDHMLK 61

QY 66 FRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALVKVRYDRDRTITILRGHSHSQITQVYG 125
DB 62 FQTGGHVPETNYIFMGDFVDRGYNSLDVFTILLKARYPANITLLRGHSHSQITQVYG 121

QY 126 FYDECLRKYGNAVWYFTDLPYLPALTALIEHIFCLHGGLSPSLDTHDHRALDRIQE 185
DB 122 FYDECLRKYGNAVWYFTDLPYLPALTALIEHIFCLHGGLSPSPDITDQIRVIERCE 181

QY 186 VPHEHGPCDLLWSDPDRCGWGISPRGAGYTFQODIAEQFNHTNGLSLVARAHQVMEGY 245

DB 182 IPHEGPPCDLWSDPEDIETWAVSPRGAGWLFGRSVTSEFNHNNLDLVC1
QY 246 NWC-QDKNVVTVFSAPNYCYRCGNMAAIMEIDETMNSFLQFEPAPROSE1
DB 242 KYMFQDKGLVTVWSAPNYCYRCGNVASILSPNENWREVKFFTTETENNQ1
QY 305 FL 306
DB 302 FL 303

RESULT 14
US-09-248-796A-18309
; Sequence 18309, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18309
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (267)
; OTHER INFORMATION: Identity of amino acid sequences at the al
US-09-248-796A-18309

Query Match 47.1%; Score 786; DB 2; Length 271;
Best Local Similarity 66.2%; Pred. No. 2e-79;
Matches 141; Conservative 32; Mismatches 40; Indels

QY 3 SYADVDRIOELSECKPLSELVKNCDOARTILVEENWVQPKVTVTC1
DB 59 SINGLDVWIEKLSCKEPLSETDVKKLCDMAVEVLQFEEVQPVQVTVIC1

QY 63 IELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALVKVRYDRDRTILR1
DB 119 MELFKIGGCPDNTNLFMGDYVDRGYYSVETVSLVCMKVFPNRTILR1

QY 123 VYGFYDECLRKYGNAVWYFTDLPYLPALTALIEHIFCLHGGLSPSLD1
DB 179 VYGFYDECLRKYGNAVWYFTDLPYLPALTALVDMKVFCWHGGLSPMIE1

QY 183 IQEVPHEHGPCDLLWSDPDRCGWGISPRGAGY 215
DB 239 IQEFPFGQCVNCWWSNSNDRKRGWYSPXKNGF 271

RESULT 15
US-09-538-092-1093
; Sequence 1093, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of U
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01

ations are unknown

; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1093
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P36873
US-09-538-092-1093

Query Match	45.3%	Score 757;	DB 2;	Length 323;
Best Local Similarity	46.3%	Pred. No. 4.6e-76;		
Matches 142;	Conservative 66;	Mismatches 87;	Indels 12;	Gaps 6;

Qy	6	DVDRIEQLSE---CKP-----LSLEVNLCDAQRTILVBEWNPVKCPVTVCDDIHG	57
Db	8	NIDSIIQRLLLEVRGSKPGKNVQLQENEIRGLCKSRREIFLSQPILLEAPLKICGDIHG	67
Qy	58	QPHDLIELFRIGGKAPDTNYLFMGDYVDRGYVSVETSLVALKVYRDRITILRGNHES	117
Db	68	QYDILLRLEFYGGFPPESNYFLGDIYDRGKQSLTIICLLAYKIKYPENFLLRGHEC	127
Qy	118	RQITQVYGFYDECLRKYGNNANWKYFTDLFDYPLTALIEHIEIFCLHGLSPSLDTLDHI	177
Db	128	ASINRIYGFYDECKERY-NIKLWKTFDFCNCLPIAAIVDEKIFCCHGGLSPDLQSQMEQI	186
Qy	178	RALDRIQSVPHGPMCDLLWSDDP-DRCGWGLSPRGAGYTFQODIAEOPNHTNGLSLVAR	236
Db	187	RRIMRPTDVPDPQGLLCDLLWSDDPKDVLGWGENDRGVSFTFGAEVYVAKFLHKHDLJLICR	246
Qy	237	AHQLVMEGYNWCQDKNVVTVFSAPNYCYRCGNMAIMEIDETMNRSLQFEPAPROSEPD	296
Db	247	AHQVVEDGYEFYFAKQQLVILFSAPNYCGEFDNAGMMSVDETLMCSFQILKPAKK-KPN	305
Qy	297	VTRK-TP 302	
Db	306	ATRPVTP 312	

Search completed: December 9, 2005, 10:25:06
Job time : 47 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 9, 2005, 10:18:01 ; Search time 119 Seconds
(without alignments)
1074.418 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MPSYADVDRQIEQLSECKPL.....EPAPROSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/us07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/us08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/us09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/us10a_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/us10b_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/us11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1670	100.0	306	3	US-09-828-302-13
2	1670	100.0	306	4	US-10-764-259-13
3	1549	92.8	306	4	US-10-236-699-22
4	1547	92.6	306	4	US-10-236-699-32
5	1521	91.1	306	4	US-10-236-699-8
6	1521	91.1	306	4	US-10-425-115-345205
7	1518	90.9	312	4	US-10-425-114-72606
8	1508.5	90.3	307	4	US-10-236-699-26
9	1508.5	90.3	307	4	US-10-437-963-143206
10	1497.5	89.7	307	4	US-10-424-599-163708
11	1486	89.0	304	5	US-10-739-930-6733
12	1483	88.8	308	4	US-10-425-115-333776
13	1470	88.0	388	4	US-10-425-115-345209
14	1454	87.1	396	4	US-10-425-115-333773
15	1427	85.4	309	4	US-10-060-065-24
16	1427	85.4	309	4	US-10-060-065-39
17	1427	85.4	309	4	US-10-059-585-45
18	1427	85.4	309	4	US-10-059-585-60
19	1427	85.4	309	5	US-10-386-971-3
20	1408	84.3	314	4	US-10-236-699-24
21	1404	84.1	311	4	US-10-236-699-3
22	1392	83.4	313	4	US-10-311-764-5
23	1392	83.4	395	4	US-10-425-115-206998
24	1389	83.2	313	4	US-10-425-115-206995
25	1388	83.1	313	6	US-11-097-143-15735
26	1388	83.1	318	4	US-10-369-493-6189
27	1385	82.9	376	4	US-10-425-114-63887

28	1382	82.8	313	4	US-10-236-699-18	Sequ
29	1381	82.7	307	4	US-10-425-115-287936	Sequ
30	1379	82.5	307	4	US-10-236-699-30	Sequ
31	1378	82.5	307	4	US-10-425-115-287051	Sequ
32	1378	82.5	327	4	US-10-425-114-56795	Sequ
33	1378	82.5	374	4	US-10-425-114-40943	Sequ
34	1375	82.3	349	4	US-10-425-115-223093	Sequ
35	1373	82.2	311	4	US-10-424-599-166855	Sequ
36	1371.5	82.1	367	4	US-10-437-963-174105	Sequ
37	1368	81.9	307	4	US-10-437-963-103935	Sequ
38	1366	81.8	314	4	US-10-424-599-191175	Sequ
39	1337.5	80.1	304	5	US-10-739-930-10910	Sequ
40	1309.5	78.4	381	4	US-10-767-701-46140	Sequ
41	1308.5	78.4	419	4	US-10-369-493-2498	Sequ
42	1291	77.3	377	3	US-09-801-368-270	Sequ
43	1291	77.3	377	4	US-10-369-493-1551	Sequ
44	1286	77.0	369	3	US-09-801-368-268	Sequ
45	1286	77.0	369	4	US-10-369-493-1568	Sequ

ALIGNMENTS

RESULT 1

US-09-828-302-13

; Sequence 13, Application US/09828302

; Patent No. US20020152502A1

; GENERAL INFORMATION:

; APPLICANT: COSTA E SILVA, OSWALDO DA

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: CHEN, ROUYING

; APPLICANT: ISHITANI, MANABU

; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND V

; TITLE OF INVENTION: IN PLANTS

; FILE REFERENCE: 16313-0029

; CURRENT APPLICATION NUMBER: US/09/828,302

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/196,001

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 13

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Physcomitrella patens

US-09-828-302-13

Query Match	100.0%	Score 1670;	DB 3;	Length 30
Best Local Similarity	100.0%	Pred. No. 7.9e-166;		
Matches 306;	Conservative 0;	Mismatches 0;	Indels	

Qy	1	MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENNVQPKCPVI	PH 60
Db	1	MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEENNVQPKCPVI	PH 60
Qy	61	DLIELFRIGGKAPTNYLFMGDYYDRGYVYVETVSLVALKVRDRITII	QI 120
Db	61	DLIELFRIGGKAPTNYLFMGDYYDRGYVYVETVSLVALKVRDRITII	QI 120
Qy	121	TQVYGFYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIFCLHGLSPS	AL 180
Db	121	TQVYGFYDECLRKYGNAVWKYFTDLFDYLPALTALIEHIFCLHGLSPS	AL 180
Qy	181	DRIEVPHGPMCDLLMSDDPDRCGWGISPRGAGYTFQDIAEQFNHTNG	QL 240
Db	181	DRIEVPHGPMCDLLMSDDPDRCGWGISPRGAGYTFQDIAEQFNHTNG	QL 240
Qy	241	VMEGYNNCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAF	RK 300
Db	241	VMEGYNNCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAF	RK 300
Qy	301	TPDYFL 306	

Db 301 TPDYFL 306

RESULT 2

US-10-764-259-13

; Sequence 13, Application US/10764259

; Publication No. US20040148658A1

GENERAL INFORMATION:

; APPLICANT: COSTA E SILVA, OSWALDO DA

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: CHEN, RUOYING

; APPLICANT: ISHITANI, MANABU

; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE

; TITLE OF INVENTION: IN PLANTS

; FILE REFERENCE: 16313-0029

; CURRENT APPLICATION NUMBER: US/10/764,259

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: 60/196,001

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Physcomitrella patens

US-10-764-259-13

Query Match 100.0%; Score 1670; DB 4; Length 306;

Best Local Similarity 100.0%; Pred. No. 7.9e-166;

Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKPVTGDIHGQFH 60

Db 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKPVTGDIHGQFH 60

Qy 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITILRGHESRQI 120

Db 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITILRGHESRQI 120

Qy 121 TOVGYFDECLRKYGANVWKYFTDLFDYLPALTALIEHIFCLHGLSPSLDTLDHIAL 180

Db 121 TOVGYFDECLRKYGANVWKYFTDLFDYLPALTALIEHIFCLHGLSPSLDTLDHIAL 180

Qy 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGSLVARAHQ 240

Db 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGSLVARAHQ 240

Qy 241 VMEGYNCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLFQEPAPRQSEPDVTRK 300

Db 241 VMEGYNCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLFQEPAPRQSEPDVTRK 300

Qy 301 TPDYFL 306

Db 301 TPDYFL 306

RESULT 3

US-10-236-699-22

; Sequence 22, Application US/10236699

; Publication No. US20030150028A1

GENERAL INFORMATION:

; APPLICANT: BOHNERT, HANS J.

; APPLICANT: CHEN, RUOYING

; APPLICANT: ISHITANI, MANABU

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: COSTA E SILVA, OSWALDO DA

; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND

; TITLE OF INVENTION: METHODS OF USE IN PLANTS

; FILE REFERENCE: 16313-0161

; CURRENT APPLICATION NUMBER: US/10/236,699

; CURRENT FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: 60/317,305

; PRIOR FILING DATE: 2001-09-05

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Glycine max

US-10-236-699-22

Query Match 92.8%; Score 1549; DB 4; Length 306

Best Local Similarity 91.5%; Pred. No. 3.7e-153;

Matches 280; Conservative 16; Mismatches 10; Indels

Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKPVT 60

Db 1 MPSHADLERQIEQLMDCKPLSESEVKALCDQARTILVEEWNVQPKPVT 60

Qy 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITIT 120

Db 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITIT 120

Qy 121 TOVGYFDECLRKYGANVWKYFTDLFDYLPALTALIEHIFCLHGLSPS 180

Db 121 TOVGYFDECLRKYGANVWKYFTDLFDYLPALTALIEHIFCLHGLSPS 180

Qy 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG 240

Db 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNG 240

Qy 241 VMEGYNCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLFQEPAP 300

Db 241 VMEGYNCQDKNVVTFVSAPNYCYRCGNMAAIMEIDETMNRSLFQEPAP 300

Qy 301 TPDYFL 306

Db 301 TPDYFL 306

RESULT 4

US-10-236-699-32

; Sequence 32, Application US/10236699

; Publication No. US20030150028A1

GENERAL INFORMATION:

; APPLICANT: BOHNERT, HANS J.

; APPLICANT: CHEN, RUOYING

; APPLICANT: ISHITANI, MANABU

; APPLICANT: VAN THIELEN, NOCHA

; APPLICANT: COSTA E SILVA, OSWALDO DA

; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE

; TITLE OF INVENTION: METHODS OF USE IN PLANTS

; FILE REFERENCE: 16313-0161

; CURRENT APPLICATION NUMBER: US/10/236,699

; CURRENT FILING DATE: 2002-09-05

; PRIOR APPLICATION NUMBER: 60/317,305

; PRIOR FILING DATE: 2001-09-05

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-236-699-32

Query Match 92.6%; Score 1547; DB 4; Length 306

Best Local Similarity 91.5%; Pred. No. 6e-153;

Matches 280; Conservative 15; Mismatches 11; Indels

Qy 1 MPSYADVDRQIEQLSECKPLSEVKNLCDQARTILVEEWNVQPKPVT 60

Db 1 MPSHADLERQIEQLMECKPLSESEVKALCDQARTILVEEWNVQPKPVT 60

Qy 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITIT 120

Db 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYYSVETVSLVALKVRDRITIT 120

QY 121 TQVYGFYDECLRKYGKGNVWKYFTDLFDYPLTALIEHIEICLHGGLSPSLDTLIDHIAL 180
 DB 121 TQVYGFYDECLRKYGKGNVWKYFTDLFDYPLTALIEHIEICLHGGLSPSLDTLIDHIAL 180
 QY 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFQGDIAEQNHTNGLSVARAHL 240
 DB 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFQGDIAEQNHTNGLSVARAHL 240
 QY 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAALMEIDETMNSFLQFEPAPQSEPDVTRK 300
 DB 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAALMEIDETMNSFLQFEPAPQSEPDVTRK 300
 QY 301 TPDYFL 306
 DB 301 TPDYFL 306

RESULT 5
 US-10-236-699-8
 ; Sequence 8, Application US/10236699
 ; Publication No. US20030150028A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOHNER, HANS J.
 ; APPLICANT: CHEN, RUOYING
 ; APPLICANT: ISHITANI, MANABU
 ; APPLICANT: VAN THIELEN, NOCHA
 ; APPLICANT: COSTA E SILVA, OSWALDO DA
 ; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
 ; TITLE OF INVENTION: METHODS OF USE IN PLANTS
 ; FILE REFERENCE: 16313-0161
 ; CURRENT APPLICATION NUMBER: US/10/236.699
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: 60/317,305
 ; PRIOR FILING DATE: 2001-09-05
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Brassica napus
 US-10-236-699-8

Query Match 91.1%; Score 1521; DB 4; Length 306;
 Best Local Similarity 88.9%; Pred. No. 3.1e-150;
 Matches 272; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MPSYADVDRQIEQLSECKPLSELVKNCDOARTILVEENNVQPKCPVT 60
 DB 1 MPETGDIRQIEQLSECKPLSELVKNCDOARTILVEENNVQPKCPVT 60
 QY 61 DLIELFRIGGKAPDTNLYFMGDYVDRGYYSVETVSLVALKVRDRITILRGHESRQI 120
 DB 61 DLIELFKTIGSSPTNLYFMGDYVDRGYYSVETVSLVALKVRDRITILRGHESRQI 120
 QY 121 TQVYGFYDECLRKYGKGNVWKYFTDLFDYPLTALIEHIEICLHGGLSPSLDTLIDHIAL 180
 DB 121 TQVYGFYDECLRKYGKGNVWKYFTDLFDYPLTALIEHIEICLHGGLSPSLDTLIDHIAL 180
 QY 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFQGDIAEQNHTNGLSVARAHL 240
 DB 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFQGDIAEQNHTNGLSVARAHL 240
 QY 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAALMEIDETMNSFLQFEPAPQSEPDVTRK 300
 DB 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAALMEIDETMNSFLQFEPAPQSEPDVTRK 300
 QY 301 TPDYFL 306
 DB 301 TPDYFL 306

RESULT 6

US-10-425-115-345205
 ; Sequence 345205, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425.115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 345205
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_77994C.1.pap
 US-10-425-115-345205

Query Match 91.1%; Score 1521; DB 4; Length 306
 Best Local Similarity 88.9%; Pred. No. 3.1e-150;
 Matches 272; Conservative 23; Mismatches 11; Indels
 s 0;
 QY 1 MPSYADVDRQIEQLSECKPLSELVKNCDOARTILVEENNVQPKCPVT 60
 DB 1 MPHADLDRQISQURDCKFLPEAEVKTLCEQAKILMEENNVQPKCPVT 60
 QY 61 DLIELFRIGGKAPDTNLYFMGDYVDRGYYSVETVSLVALKVRDRITIT 120
 DB 61 DLIELFRIGGKAPDTNLYFMGDYVDRGYYSVETVSLVALKVRDRITIT 120
 QY 121 TQVYGFYDECLRKYGKGNVWKYFTDLFDYPLTALIEHIEICLHGGLSP 180
 DB 121 TQVYGFYDECLRKYGKGNVWKYFTDLFDYPLTALIEHIEICLHGGLSP 180
 QY 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFQGDIAEQNHTNG 240
 DB 181 DRIQVPEHGPMDLLWSDPDDRCGWGISPRGAGYTFQGDIAEQNHTNG 240
 QY 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAALMEIDETMNSFLQFEPAF 300
 DB 241 VMEGYNWQDKNNVTVFSAPNYCYRCGNMAALMEIDETMNSFLQFEPAF 300
 QY 301 TPDYFL 306
 DB 301 TPDYFL 306

RESULT 7
 US-10-425-114-72606
 ; Sequence 72606, Application US/10425114
 ; Publication No. US2004003488A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improv
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425.114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72606
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Zea mays subsp. mexicana
 ; FEATURE:

ated With

RESULT 10
US-10-424-599-163708
; Sequence 163708, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 163708
LENGTH: 307
TYPE: PRT
ORGANISM: Glycine max
NAME/KEY: unsure
LOCATION: (1)..(307)
OTHER INFORMATION: unsure at all Xaa locations
OTHER INFORMATION: unsure at all Xaa locations
US-10-424-599-163708

Query Match 89.7%; Score 1497.5; DB 4; Length 307;
Best Local Similarity 88.6%; Pred. No. 9.1e-148;
Matches 272; Conservative 16; Mismatches 18; Indels 1; Gaps 1;
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVTVCGDHGOFP 60
DB 1 MPSHADLERQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVTVCGDHGOFP 60
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITILRGHNSRQI 120
DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITILRGHNSRQI 120
QY 121 TQVGYFDECLRKYGNNVWYFTDLFDYPLTLALIEHIEIFCLHGLSPSLDLTHIRA 179
DB 121 TQVGYFDECLRKYGNNVWYFTDLFDYPLTLALIEHIEIFCLHGLSPSLDLTHIRA 180
QY 180 LDRIQEVPHGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSVARHQ 239
DB 181 LDRIQEVPHGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLISRAHQ 240
QY 240 LVMEGYNWCQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFPAQSEPDVTR 299
DB 241 LVMEGYNWCQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFPAQSEPDVTR 300
QY 300 KTPDYFL 306
DB 301 KTPDYFL 307

RESULT 11
US-10-739-930-6733
Sequence 6733, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 6733
LENGTH: 304
TYPE: PRT
ORGANISM: Arabidopsis thaliana
NAME/KEY: unsure
LOCATION: (1)..(304)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:

OTHER INFORMATION: Clone ID: ARATH-23APR03-C8015_1.p
US-10-739-930-6733
Query Match 89.0%; Score 1486; DB 5; Length 304
Best Local Similarity 88.2%; Pred. No. 1.4e-146;
Matches 270; Conservative 16; Mismatches 18; Indels
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
DB 1 MPSNGDLDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
QY 121 TQVGYFDECLRKYGNNVWYFTDLFDYPLTLALIEHIEIFCLHGLSPS
DB 121 T--XGYFDECLRKYGNNVWYFTDLFDYPLTLALIEHIEIFCLHGLSPS
QY 181 LDRIQEVPHGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGL
DB 179 LDRIQEVPHGPMCDLLWSDPDDRCGWGISPRGAGYTFGQDIAEQFNHTNGL
QY 241 LVMEGYNWCQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFPAF
DB 239 LVMEGYNWCQDKNNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFPAF
QY 301 TPDYFL 306
DB 299 TPDYFL 304

RESULT 12
US-10-425-115-333776
Sequence 333776, Application US/104251115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 333776
LENGTH: 308
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(308)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_67515C.1.p
US-10-425-115-333776

Query Match 88.8%; Score 1483; DB 4; Length 308
Best Local Similarity 87.0%; Pred. No. 3e-146;
Matches 268; Conservative 24; Mismatches 14; Indels
QY 1 MPSYADVDRQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
DB 1 MPSHGDLDRLQIEQLSECKPLSEVKNLDCQARTILVEEWNVPVKCPVT
QY 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
DB 61 DLIELFRIGGKAPDNTNLFMGDYVDRGYVETVSLVALLVVKVYRDRITIT
QY 121 TQVGYFDECLRKYGNNVWYFTDLFDYPLTLALIEHIEIFCLHGLSPS
DB 121 TQVGYFDECLRKYGNNVWYFTDLFDYPLTLALIEHIEIFCLHGLSPS

APPLICANT: Shizuko Ishii
APPLICANT: Tomoyasu Sugiyama
APPLICANT: Ai Wakamatsu
APPLICANT: Keiichi Nagai
APPLICANT: Tetsuji Otsuki
APPLICANT: Shin-ichi Funahashi
APPLICANT: Chiaki Sencoo
APPLICANT: Jun-ichi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
CURRENT APPLICATION NUMBER: US/10/060,065
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05061
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-065-24

Query Match 85.4%; Score 1427; DB 4; Length 309;
Best Local Similarity 83.7%; Pred. No. 2.2e-140;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

Qy	6	DVDRQIEQLSECKPLSELEVENLDCQARTILVEENWVQPKCPVTCGDIHGQFHDLEL	65
Db	9	ELDQWIEQLNECKQLSESKLCEKAEILTKESNVQEVRCPTVCGDVHGQFHDLMEL	68
Qy	66	FRIGGKAPDTNLYFMGDYVDRGYYSVETVSLVALVKVRYRDRITILRGNHESRQITQVYG	125
Db	69	FRIGGKSPDTNLYFMGDYVDRGYYSVETVLLVALKVRYRERITILRGNHESRQITQVYG	128
Qy	126	FYDECLRYKGNANVWKYFTDLFDYLPALTALIEHEIFCLHGLSPSLDTLDIRALDRIOE	185
Db	129	FYDECLRYKGNANVWKYFTDLFDYLPALTALVDGQIFCLHGLSPSIDTLDIRALDRIOE	188
Qy	186	VPHGPMCDLLWSDDRCGWGISPRGAGYTFGODIAEQENHTNGLSLAVARAHQLVMEGY	245
Db	189	VPHGPMCDLLWSDDRCGWGISPRGAGYTFGQDISETFNLANGTLVSRAHQLVMEGY	248
Qy	246	NWCODKNVTVFSAFNYCYRCGNMAAIMEIDETWNRSLQEPAPROSEPQVTRKTPDYF	305
Db	249	NWCHDRNVTVFSAFNYCYRCGNQAAINELDDTLKYSFLQFDPAPRGCEPHVTRTPDYF	308
Qy	306	L 306	
Db	309	L 309	

Search completed: December 9, 2005, 10:27:17
Job time : 120 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 10:20:31 ; Search time 38 Seconds
(without alignments)
44.969 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MFSYADVDRQIEQLSECKPL.....BPAPRQSPDVTRKTPDYFL 306

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1427	85.4	309	7 US-11-109-156-24	Sequence 24, Appl
2	1427	85.4	309	7 US-11-109-156-39	Sequence 39, Appl
3	757	45.3	319	7 US-11-109-156-38	Sequence 38, Appl
4	757	45.3	323	6 US-10-878-556A-184	Sequence 184, Appl
5	757	45.3	323	7 US-11-109-156-37	Sequence 37, Appl
6	565	33.8	521	7 US-11-109-156-34	Sequence 34, Appl
7	87.5	5.2	276	6 US-10-467-657-2502	Sequence 2502, Ap
8	87	5.2	250	7 US-11-135-855-41	Sequence 41, Appl
9	76.5	4.6	316	6 US-10-485-517-370	Sequence 370, Appl
10	76.5	4.6	696	7 US-11-029-003-8	Sequence 8, Appl
11	76	4.6	264	6 US-10-467-657-6940	Sequence 6940, Ap
12	75.5	4.5	677	7 US-11-058-727-52	Sequence 52, Appl
13	75.5	4.5	677	7 US-11-058-727-84	Sequence 84, Appl
14	75.5	4.5	677	7 US-11-108-389-52	Sequence 52, Appl
15	75.5	4.5	677	7 US-11-108-389-84	Sequence 84, Appl
16	74.5	4.5	459	6 US-10-793-626-1246	Sequence 1246, Ap
17	74.5	4.5	459	6 US-10-793-626-2554	Sequence 2554, Ap
18	74	4.4	518	6 US-10-793-626-506	Sequence 506, Appl
19	72.5	4.3	267	7 US-10-495-597-5	Sequence 5, Appl
20	72.5	4.3	673	7 US-11-058-727-14	Sequence 14, Appl
21	72.5	4.3	673	7 US-11-108-389-14	Sequence 14, Appl
22	72.5	4.3	1210	7 US-11-058-727-4	Sequence 4, Appl
23	72.5	4.3	1210	7 US-11-108-389-4	Sequence 4, Appl
24	72	4.3	406	6 US-10-770-726-73	Sequence 73, Appl
25	71.5	4.3	472	6 US-10-689-742-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-11-109-156-24
; Sequence 24, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTE

TITLE OF INVENTION: PHOSPHATASE

FILE REFERENCE: 06501-099002

CURRENT APPLICATION NUMBER: US/11109,156

PRIOR FILING DATE: 2005-04-19

PRIOR APPLICATION NUMBER: US/10/060,065

PRIOR FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05061

PRIOR FILING DATE: 2000-07-28

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR FILING DATE: 1999-10-18

PRIOR APPLICATION NUMBER: US 60/183,322

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: JP 11-248036

PRIOR FILING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: JP 2000-118776

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: JP 2000-183767

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: JP 2000-241899

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 24

LENGTH: 309

TYPE: PRT

ORGANISM: Homo sapiens

US-11-109-156-24

Query Match 85.4%; Score 1427; DB 7; Length 309;
Best Local Similarity 83.7%; Pred. No. 4.8e-132;
Matches 252; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

QY 6 DVDROIQLSECKPLSELEVNKLCDQARTILVEENVQPKPVTCGDHGHQFDLIEL 65
DB 9 ELDDWIEQLNECKQLSESQVKSCLCEKAEILTKESNVQEVRCPTVTCGDHLMEL 68

QY 66 FRIGKAPDNTNLFMGDYVDRGYYSVETVSLVALVKVRYRDRITILRGHNSRQITQVYG 125
DB 69 FRIGKSPDNTNLFMGDYVDRGYYSVETVTLVALVKVRYRDRITILRGHNSRQITQVYG 128

QY 126 FYDECLRYGNANWKYFTDLFDYLPALTALIEHIFCLHGGSLPSLIDLRALDRIOE 185
DB 129 FYDECLRYGNANWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSLIDLRALDRIOE 188

QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSVARAHQLVMEGY 245
DB 189 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNHANGLTVSRAHQLVMEGY 248

QY 246 NWCQDKNVVTFPSAPNYCYRCGNMAAIMEIDETMNRSELOFEPAPROQSEPDVTRKTPDYF 305
DB 249 NWCHDRNVVTFPSAPNYCYRCGNMAAIMEIDETMNRSELOFEPAPRGEPHVTRTRTPDYF 308

QY 306 L 306
DB 309 L 309

RESULT 2
US-11-109-156-39
; Sequence 39, Application US/11109156
; Publication NO. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 2000-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 309

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-39

Query Match 85.4%; Score 1427; DB 7; Length 309
Best Local Similarity 83.7%; Pred. No. 4.8e-132;
Matches 252; Conservative 32; Mismatches 17; Indels 0;

QY 6 DVDROIQLSECKPLSELEVNKLCDQARTILVEENVQPKPVTCGDHGHQFDLIEL 65
DB 9 ELDDWIEQLNECKQLSESQVKSCLCEKAEILTKESNVQEVRCPTVTCGDHLMEL 68

QY 66 FRIGKAPDNTNLFMGDYVDRGYYSVETVSLVALVKVRYRDRITILRGHNSRQITQVYG 125
DB 69 FRIGKSPDNTNLFMGDYVDRGYYSVETVTLVALVKVRYRDRITILRGHNSRQITQVYG 128

QY 126 FYDECLRYGNANWKYFTDLFDYLPALTALIEHIFCLHGGSLPSLIDLRALDRIOE 185
DB 129 FYDECLRYGNANWKYFTDLFDYLPALTALVDGQIFCLHGGSLPSLIDLRALDRIOE 188

QY 186 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDIAEQFNHTNGLSVARAHQLVMEGY 245
DB 189 VPHEGPMCDLLWSDPDDRCGNGISPRGAGYTFGQDISETFNHANGLTVSRAHQLVMEGY 248

QY 246 NWCQDKNVVTFPSAPNYCYRCGNMAAIMEIDETMNRSELOFEPAPROQSEPDVTRKTPDYF 305
DB 249 NWCHDRNVVTFPSAPNYCYRCGNMAAIMEIDETMNRSELOFEPAPRGEPHVTRTRTPDYF 308

QY 306 L 306
DB 309 L 309

RESULT 3
US-11-109-156-38
; Sequence 38, Application US/11109156
; Publication NO. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-Ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-Ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-Ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09

QY	178	RALDRIQVPHGPMCDLLWSDDP--DRCGWGISPRGAGYTFGQDIABQFN	QY	178	RALDRIQVPHGPMCDLLWSDDP--DRCGWGISPRGAGYTFGQDIABQFN	AR 233
DB	187	RRIMEPTDVPDQGLLCDLLWSDDPDKDVLGWSGENDRGVSFTFGAEVAKFI	DB	187	RRIMEPTDVPDQGLLCDLLWSDDPDKDVLGWSGENDRGVSFTFGAEVAKFI	CR 246
QY	237	AHOLVMEGVNMCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQF	QY	237	AHOLVMEGVNMCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQF	PD 296
DB	247	AHQVVEDGYEFAKRLQVTLFSAPNYCGEFDNAGNMSVDETLNCSFOIL	DB	247	AHQVVEDGYEFAKRLQVTLFSAPNYCGEFDNAGNMSVDETLNCSFOIL	PN 305
QY	297	VTRK-TP 302	QY	297	VTRK-TP 302	
DB	306	ATRPVTP 312	DB	306	ATRPVTP 312	
<p>RESULT 5</p> <p>US-11-109-156-37</p> <p>Sequence 37, Application US/11109156</p> <p>Publication No. US20050250144A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Toshio Ota</p> <p>APPLICANT: Takao Isogai</p> <p>APPLICANT: Tetsuo Nishikawa</p> <p>APPLICANT: Koji Havaashi</p> <p>APPLICANT: Kaoru Otsuka</p> <p>APPLICANT: Jun-Ichi Yamamoto</p> <p>APPLICANT: Shizuko Ishii</p> <p>APPLICANT: Tomoyasu Sugiyama</p> <p>APPLICANT: Ai Wakamatsu</p> <p>APPLICANT: Keiichi Nagai</p> <p>APPLICANT: Tetsuji Otsuki</p> <p>APPLICANT: Shin-Ichi Funahashi</p> <p>APPLICANT: Chiaki Senoo</p> <p>APPLICANT: Jun-Ichi Nezu</p> <p>TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTE</p> <p>FILE REFERENCE: 06501-099002</p> <p>CURRENT APPLICATION NUMBER: US/11/109,156</p> <p>CURRENT FILING DATE: 2005-04-19</p> <p>PRIOR APPLICATION NUMBER: US/10/060,065</p> <p>PRIOR FILING DATE: 2002-01-29</p> <p>PRIOR APPLICATION NUMBER: PCT/JP00/05061</p> <p>PRIOR FILING DATE: 2000-07-28</p> <p>PRIOR APPLICATION NUMBER: US 60/159,590</p> <p>PRIOR FILING DATE: 1999-10-18</p> <p>PRIOR APPLICATION NUMBER: US 60/183,322</p> <p>PRIOR FILING DATE: 2000-02-17</p> <p>PRIOR APPLICATION NUMBER: JP 11-248036</p> <p>PRIOR FILING DATE: 1999-07-29</p> <p>PRIOR APPLICATION NUMBER: JP 2000-118776</p> <p>PRIOR FILING DATE: 2000-01-11</p> <p>PRIOR APPLICATION NUMBER: JP 2000-183767</p> <p>PRIOR FILING DATE: 2000-05-02</p> <p>PRIOR APPLICATION NUMBER: JP 2000-241899</p> <p>PRIOR FILING DATE: 2000-06-09</p> <p>NUMBER OF SEQ ID NOS: 43</p> <p>SOFTWARE: PatentIn Ver. 2.0</p> <p>SEQ ID NO 37</p> <p>LENGTH: 323</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-11-109-156-37</p>						
QY	6	DVDRIOELSE---CKP-----LSELVKNLCDQARTILVEEWNVPVKPVTTCGDIHG 57	QY	6	DVDRIOELSE---CKP-----LSELVKNLCDQARTILVEEWNVPVKPVTTCGDIHG 57	
DB	4	NIDSIIQRLLEVRGSKPKGNVOLQENIRGLSKRSREIFUSQPIILLEAPLKTCGDIHG 63	DB	4	NIDSIIQRLLEVRGSKPKGNVOLQENIRGLSKRSREIFUSQPIILLEAPLKTCGDIHG 63	
QY	58	QPHDLIELFRIGGKAPDNTNLFMGDYVDRGVYSVETVSLVALVKVRYDRDITILRGNHES 117	QY	58	QPHDLIELFRIGGKAPDNTNLFMGDYVDRGVYSVETVSLVALVKVRYDRDITILRGNHES 117	
DB	64	QYIDLRLFEYGGFPESNYFLGDYVDRGQSLETICLLAYKIKYPENFFLLRGNHEC 123	DB	64	QYIDLRLFEYGGFPESNYFLGDYVDRGQSLETICLLAYKIKYPENFFLLRGNHEC 123	
QY	118	ROITQVGYDECLRYGNANWKYFTDLFDYLPPLTALIEHIEIFCLRGGLSPSLDTLDHI 177	QY	118	ROITQVGYDECLRYGNANWKYFTDLFDYLPPLTALIEHIEIFCLRGGLSPSLDTLDHI 177	
DB	124	ASINRIYGYDECKRY-NIKLWTKTDFCNCLPTAAIVDEKIFCCHGGLSPDLSQMEQI 182	DB	124	ASINRIYGYDECKRY-NIKLWTKTDFCNCLPTAAIVDEKIFCCHGGLSPDLSQMEQI 182	
QY	178	RALDRIQVPHGPMCDLLWSDDP--DRCGWGISPRGAGYTFGQDIABQFNHNGLSVAR 236	QY	178	RALDRIQVPHGPMCDLLWSDDP--DRCGWGISPRGAGYTFGQDIABQFNHNGLSVAR 236	
DB	183	RRIMEPTDVPDQGLLCDLLWSDDPDKDVLGWSGENDRGVSFTFGAEVAKFLHKKHDLIDICR 242	DB	183	RRIMEPTDVPDQGLLCDLLWSDDPDKDVLGWSGENDRGVSFTFGAEVAKFLHKKHDLIDICR 242	
QY	237	AHOLVMEGVNMCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPD 296	QY	237	AHOLVMEGVNMCODKNVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAPROSEPD 296	
DB	243	AHQVVEDGYEFAKRLQVTLFSAPNYCGEFDNAGNMSVDETLNCSFOILKPAEKK-KPN 301	DB	243	AHQVVEDGYEFAKRLQVTLFSAPNYCGEFDNAGNMSVDETLNCSFOILKPAEKK-KPN 301	
QY	297	VTRK-TP 302	QY	297	VTRK-TP 302	
DB	302	ATRPVTP 308	DB	302	ATRPVTP 308	
<p>RESULT 4</p> <p>US-10-878-556A-184</p> <p>Sequence 184, Application US/10878556A</p> <p>Publication No. US20050266399A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Hoffmann La-Roche Inc.</p> <p>TITLE OF INVENTION: HCV regulated protein expression</p> <p>FILE REFERENCE: 21762</p> <p>CURRENT APPLICATION NUMBER: US/10/878,556A</p> <p>CURRENT FILING DATE: 2004-06-28</p> <p>NUMBER OF SEQ ID NOS: 199</p> <p>SOFTWARE: PatentIn version 3.1</p> <p>SEQ ID NO 184</p> <p>LENGTH: 323</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>PUBLICATION INFORMATION:</p> <p>DATABASE ACCESSION NUMBER: sw_hum/pplg_human</p> <p>DATABASE ENTRY DATE: 1994-06-01</p> <p>US-10-878-556A-184</p>						
QY	6	DVDRIOELSE---CKP-----LSELVKNLCDQARTILVEEWNVPVKPVTTCGDIHG 57	QY	6	DVDRIOELSE---CKP-----LSELVKNLCDQARTILVEEWNVPVKPVTTCGDIHG 57	
DB	8	NIDSIIQRLLEVRGSKPKGNVOLQENIRGLSKRSREIFUSQPIILLEAPLKTCGDIHG 67	DB	8	NIDSIIQRLLEVRGSKPKGNVOLQENIRGLSKRSREIFUSQPIILLEAPLKTCGDIHG 67	
QY	58	QPHDLIELFRIGGKAPDNTNLFMGDYVDRGVYSVETVSLVALVKVRYDRDITILRGNHES 117	QY	58	QPHDLIELFRIGGKAPDNTNLFMGDYVDRGVYSVETVSLVALVKVRYDRDITILRGNHES 117	
DB	68	QYIDLRLFEYGGFPESNYFLGDYVDRGQSLETICLLAYKIKYPENFFLLRGNHEC 127	DB	68	QYIDLRLFEYGGFPESNYFLGDYVDRGQSLETICLLAYKIKYPENFFLLRGNHEC 127	
QY	118	ROITQVGYDECLRYGNANWKYFTDLFDYLPPLTALIEHIEIFCLRGGLSPSLDTLDHI 177	QY	118	ROITQVGYDECLRYGNANWKYFTDLFDYLPPLTALIEHIEIFCLRGGLSPSLDTLDHI 177	
DB	128	ASINRIYGYDECKRY-NIKLWTKTDFCNCLPTAAIVDEKIFCCHGGLSPDLSQMEQI 186	DB	128	ASINRIYGYDECKRY-NIKLWTKTDFCNCLPTAAIVDEKIFCCHGGLSPDLSQMEQI 186	

Qy	118	ROITQVGYGYSCLARKYGNANVWKYFTDLPYLPALTALIEHETPC LHGGLSPLSDLTLDHI	177
Db	128	ASINRIYGYDECKERY-NIKLWKTFTDFCNCLPTAAIVDEKIPCCHGGLSPDLQSMEQI	186
Qy	178	RALDRLOEYVPHGSPWCDLLWSDDP-DRCGWGISPRGAGYTFGODIAEQFNHTNGLSIVAR	236
Db	187	RRIMRPTDVPDQGLCDLLWSDDPKDVLGWGENDRGVSFTFGAEVWAKFLHGHLDOLI	246
Qy	237	AHOLVMGYNWCQDKNVTVFSAPNYCYRCGNMAIMEIDETMNRSLQTEPAPROSEPD	296
Db	247	AHQVVEDGEYFAKRLQVLTLFSAPNYCGEFDNAGAMMSVDETLMCSFOILKPAEKK-KPN	305
Qy	297	VTRK-Tp	302
Db	306	ATSPVTP	312

```

RESULT 6
US-11-109-156-34
; Sequence 34, Application US/1109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; TITLE OF INVENTION: PHOSPHATASE
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-34

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Qy      80  MGDYVDRGYYSVETSLVALLKVKRYRDRITILRGNHESROIQTQVGYFYDE
Db      116  LGDYVDRGYFIECVLYLWALKILYPKTLFLLRGNHECRHLTEYTFYFKQE
Qy      140  WKYFTDLFDYLPLTALIEHIEIFCLHGGLSPLDTLDHIRALDRLOEVPHE
Db      175  YDAMDAFDCLPLAALMNQOFLCVHGLSPSEINTLDDIRKLDRFKPEPAY
Qy      200  PDRDRCG-----WGISPRGAGYTFQDIAEOFNHTNGISLVARAHQIVI
Db      235  PLEDGNEKTEQHEHTNTVRCGSFYFSYPACVCEFLQHNNLLSIURAHEAQI
Qy      252  -----NVVTVFSAPNYCYRCGNMAAIMEIDETMNRSLQFEPAP 290
Db      295  QTTGFSLIITIFAPNVLVDYNNKAAVLKYENNVMNIROFNCSF 338

RESULT 7
US-10-467-657-2502
; Sequence 2502, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2502
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2502

```

```

RESULT 8
US-11-1335-855-41
; Sequence 41, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/1335,855

```

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; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-41

Query Match          5.2%; Score 87; DB 7; Length 250;
Best Local Similarity 22.1%; Pred. No. 0.13;
Matches 49; Conservative 29; Mismatches 80; Indels 64; Gaps 11;

Qy      111  LRGNHESRQITQVGYFVDECLRYKRNA-----NVKYYTDLFLYPLTALIEHIFCLHG 165
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      28   MNAKHKRVSPSPDKLYEECIIPWKDNACCTLTTSWE-----AHLDSVLYNFSLF--HC 79

Qy      166  GLSPSLDTLHDHIALDRIQEVPHGPMCDLLWSDPPDCRGWGISPRCAG-----YTFGQD 220
          |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      80  GLLMPGCRKHFIQATCYECSNLGP-----WIVGSLGWVAFSPQGGERVVNVPLCQE 134
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Qy      221  IAEQFNHTNGLSLVARAHLVMBGYNWCQDNVVTVFSAPNYCVRCCNMAAIMEI----- 275
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      135  DCEEWEDCRMYSYTKSNW---RGWDWSQGN-----RCPKGAQCLPFSHYFP 180

Qy      276  -----DETWNRRF-----LQ--FEPAPRQSEPDV 297
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

Db      181  TPADLGKXTWSNFKASPERRNSGRCLQKWFEPA--QGNPNV 220
          :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

```

```

RESULT 9
US-10-485-517-370
; Sequence 370, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 370
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-370

Query Match          4.6%; Score 76.5; DB 6; Length 316;
Best Local Similarity 20.3%; Pred. No. 1.9;
Matches 55; Conservative 43; Mismatches 60; Indels 113; Gaps 17

QY      1  MPSYADVDRIQEQLS-ECKPLS-----ELEVKMLCQAARTIL-----VE 38
      68  MNSYA-VDETIGLAKQCKQYESQILNLYTGLNIEAIFQIAETLAKSKVDGIVLMATDIT 126
      39  EWNQPV---KCPVTTCGDIHQFHDILI-ELFRIGGKAPPTNYLFMGDYV-DRGYYSVET 93
      QY      EWNQPV---KCPVTTCGDIHQFHDILI-ELFRIGGKAPPTNYLFMGDYV-DRGYYSVET 93

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Qy 269 MAATMEIDETMNRSLQFEPAPRQSEPDVTRKTP 302
| : | : : : :
Dd 575 KALPAPIEKTISKAKGPR--EPQVYTLPP 602

RESULT 11

```

US-10-467-657-6940
; Sequence 6940, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6940
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6940

```

	Query Match	4.6%; Score 76; DB 6; Length 264;
	Best Local Similarity	22.5%; Pred.No 1.7;
	Matches	36; Conservative 18; Mismatches 60; Indels 46; Gaps 8;
Qy	125 GFYDECLRKYGNNVWVFDTLPD-----LPTALIEHIEICLGGLSPSLDTLDHI	177
Db	: : : : : : : : : : : : : : : : : :	
	65 GMLSALQKQISANYW-LFNDCVRSLRAEKLPOS----PDFYCGDAENFFFORQDFDLI	119
Qy	178 RALDRIGEVPEHGPMCDLLMSDPD-----RCGWSISPRG--AGYTFGDQIAEACNHNHTNGL	231
Db	: : : : : : : : : : : : : : : : : :	
	120 ASASAVQ-----WFHQPDFAFHCKTGLKTGNLLAVATFGKNLKEVRLQITNI	167
Qy	232 SL-----VARAHQLVMGYNNQCQRNVVTVSAP	260
Db	: : : : : : : : : : : : : : : : : :	
	168 GLNYPTLSOWMAAKXDFELL-----WCEPFKVILDDTP	202

RESIST 12

```

US-11-058-727-52
; Sequence 52, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Preenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134

```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 677
; TYPE: PRF
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-52
```

	Query Match	4.5%; Score 75.5; DB 7; Length 677
	Best Local Similarity	17.4%; Pred.No. 6.4;
	Matches	70; Conservative 63; Mismatches 128; Indels 1.
Qy	7 VDRQIEQLSECKPLSLELVKNLGDQARTILVEEWNVPVKCPVTCG-- :: :: : :	
Dd	123 INKIAIYARKALSELGLEGNKYQLYLTALEEWEENPFRSRGLSGRP; : : : :	
Qy	61 DLIELF-----RIGKAPDNTNYLFMGD---VVDRGYYS :	
Dd	183 ILDSLFTQYMPSPRVTNFEVPFLTVVAMAANLLHLLLKDASIFGEWGS' : : : :	
Qy	101 KVRYPDRIITLRGNHSROITOVVGPFDECLRY-----GNANVWK : : : :	
Dd	238 -----NYDRQMKLTAEYSDHCXKWYETGLAKLGTS AKOWIV : : : :	
Qy	152 LTALIHEIFECLHGGLSPSLDTLDHIRALDRIOEPHEGMCDLLWSDDPD : : : :	
Dd	285 LAVLDVVALLF-----PNVDT-----RTYPEMKAQLTREYYTDPLA : : : :	
Qy	212 GAGY----TFQGDIABEQ-----FNHTNGLSLVARA----- : : : :	
Dd	328 GSUYDKAPSFG--VIESSVIPRHVFDFYTGLTYVTSQRSISSARYIRHW. : : : :	
Qy	241 ----VMEGYNWCQDNKVTVFSAPNP-CYRCGNMAAIM----- : : : :	
Dd	386 SRGSNLQQMYGTQNHLSTSFDTFTNVDYIKTLSKDAVLIDIVYPGYTI: : : : :	
Qy	279 M-----NRSLFOPEP-----APROSE---PDVTRKTDPY 304 : : : :	
Dd	446 MVNOLNNRKTLKYNPVSKOIIASTRSDELSEPETSODQNP 487 : : : :	

PRECIT. 13

```

RESULI 13
US-11-058-727-84
; Sequence 84, Application US/11058727
; Publication No. US20050261483A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Preenail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins with Pesticidal
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 35718/287809
; CURRENT APPLICATION NUMBER: US/11/058,727
; CURRENT FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/460,787
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-058-727-84

```

Query Match 4.5%; Score 75.5; DB 7; Length 677;
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;

QY 7 VDRQIEQLSECKPLSELEVNLCQARTILVEWNVQPKVTCG-----DTHGQFH 60
DB 123 INQKIAEYARNKALSEGLEGNYYQLYLTALBEEBENPFRSGSLNGSRPALRDVNRNFE 182

QY 61 DLIELF-----RIGGKAPDNTNLYLFMGD---YVDRGYYSVETVSLVAL 100
DB 183 ILDSLFTQYMPSPRVTFNEVPLTVYMAANLHLLKADASIFGEWGWSTTIN----- 237

QY 101 KVRVDRITILRGHESRQITQVGYFDECLRY-----GNANVWKYFTDLFDYLP 151
DB 238 -----NYDRQMKLTAEYSDHCVKWYETGLAKGTSAKQWVDVYQFRREMT 284

QY 152 LTALIEHETFCFLHGLGSLDRLDRIQVPHGPMCDLLWSDDRCGHSIPR 211
DB 285 LAVLDVVALF-----PNYDT-----RYPMETKAQLTRVYTDPLGAV--NVSSI 327

QY 212 GAGY----TFGQDIAEQ-----FNHTNGLSLVARA-----HQL----- 240
DB 328 GSWYDKAPSGF--VLESSVIRPPHVDYITGLTVVYQTSRSISSARYIRHWAGHQSIRHV 385

QY 241 -----VMEGYNCQDNVVVFSAPNY-CYRCGNMAAIM-----EIDET 278
DB 386 SRGSNLQOMYGTNQNLHSTSTFDTNYYIKTSLKDAVLLDIVYPGYTVIFGMEVEVFF 445

QY 279 M-----NRSFLOPEP-----APROSE---PDVTRKTPDY 304
DB 446 MVNQLNTRKTLKYNPVSVDIIASTRDSELELPPEPETSQPNY 487

RESULT 14
US-11-108-389-52
; Sequence 52, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-52

Query Match 4.5%; Score 75.5; DB 7; Length 677;
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 141; Gaps 18;

QY 7 VDRQIEQLSECKPLSELEVNLCQARTILVEWNVQPKVTCG-----DTHGQFH 60
DB 123 INQKIAEYARNKALSEGLEGNYYQLYLTALBEEBENPFRSGSLNGSRPALRDVNRNFE 182

QY 61 DLIELF-----RIGGKAPDNTNLYLFMGD---YVDRGYYS
DB 183 ILDSLFTQYMPSPRVTFNEVPLTVYMAANLHLLKADASIFGEWGWSE
QY 101 KVRVDRITILRGHESRQITQVGYFDECLRY-----GNANVWK
DB 238 -----NYDRQMKLTAEYSDHCVKWYETGLAKLTGTSKQWV
QY 152 LTALIEHETFCFLHGLGSLDRLDRIQVPHGPMCDLLWSDDL
DB 285 LAVLDVVALF-----PNYDT-----RYPMETKAQLTRVYTDPL
QY 212 GAGY----TFGQDIAEQ-----FNHTNGLSLVARA-----
DB 328 GSWYDKAPSGF--VLESSVIRPPHVDYITGLTVVYQTSRSISSARYIRHW
QY 241 -----VMEGYNCQDNVVVFSAPNY-CYRCGNMAAIM-----
DB 386 SRGSNLQOMYGTNQNLHSTSTFDTNYYIKTSLKDAVLLDIVYPGYTYI
QY 279 M-----NRSFLOPEP-----APROSE---PDVTRKTPDY 304
DB 446 MVNQLNTRKTLKYNPVSVDIIASTRDSELELPPEPETSQPNY 487

RESULT 15
US-11-108-389-84
; Sequence 84, Application US/11108389
; Publication No. US20050261188A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Ronald D. Flannagan
; APPLICANT: Rafael Herrmann
; APPLICANT: Theodore W. Kahn
; APPLICANT: Albert L. Lu
; APPLICANT: Billy Fred McCutchen
; APPLICANT: James K. Presnail
; APPLICANT: James F.H. Wong
; APPLICANT: Cao-Guo Yu
; TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
; FILE REFERENCE: 35718/291049
; CURRENT APPLICATION NUMBER: US/11/108,389
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/391,786
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/606,320
; PRIOR FILING DATE: 2003-06-25
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-108-389-84

Query Match 4.5%; Score 75.5; DB 7; Length 677
Best Local Similarity 17.4%; Pred. No. 6.4;
Matches 70; Conservative 63; Mismatches 128; Indels 1

QY 7 VDRQIEQLSECKPLSELEVNLCQARTILVEWNVQPKVTCG---
DB 123 INQKIAEYARNKALSEGLEGNYYQLYLTALBEEBENPFRSGSLNGSRF
QY 61 DLIELF-----RIGGKAPDNTNLYLFMGD---YVDRGYYS
DB 183 ILDSLFTQYMPSPRVTFNEVPLTVYMAANLHLLKADASIFGEWGWSE
QY 101 KVRVDRITILRGHESRQITQVGYFDECLRY-----GNANVWK
DB 151

1	1670	100.0	1365	6	ABN81332	Abn81332 Physcomit
2	1670	100.0	1365	8	ABX16239	Abx16239 P. patens
3	1549	92.8	1386	10	ACC43349	Acc43349 Protein 1
4	1547	92.6	1330	10	ACC43354	Acc43354 Protein 1

PA (BADI) BASF PLANT SCI GMBH.
XX Da Costa E SilvaO, Bohnert HJ, Ishitani M, Van Thielen N, Chan R;
XX WPI; 2002-508562/54.
XX P-PSDB; ABB77578.
XX New transgenic plant cell transformed by phosphatase stress-related
PT protein coding nucleic acid whose expression in the cell results in
PT increased tolerance to environmental stress compared to wild type cell.
XX Claim 18; Fig 2; 106pp; English.
XX The invention relates to a transgenic plant cell (I) transformed by a
CC phosphatase stress-related protein (PHSRP) coding nucleic acid (ABN81330-
CC ABN81334), where expression of the nucleic acid in the plant cell results
CC in increased tolerance to an environmental stress as compared to a wild
CC type variety of the plant cell. PHSRP encoding genes are useful for
CC identifying Physcomitrella patens and related organisms, as markers for
CC specific regions of the genome, mapping of genomes of organisms related
CC to P. patens, identification and localisation of P. patens sequences of
CC interest, evolutionary studies, determination of PHSRP regions required
CC for function, modulation of a PHSRP activity, modulation of the
CC metabolism of one or more cell functions, modulation of the transmembrane
CC transport of one or more compounds and modulation of stress resistance.
CC The gene is also useful for identifying and/or cloning PHSRP homologues
CC in other cell types and organisms, for identifying an organism as being
CC P. patens or its close relative and for evolutionary and protein
CC structural studies. The present sequence is that of a PHSRP encoding
CC polynucleotide of the invention
XX
SQ Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9, 72e-180 Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-764-259-13 (1-306) x ABN81332 (1-1365)
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
Db 71 ATGCGTGCATATGAGATGATAGACCGGAGATAGACGAGCTGCGAGTGCAGGCGGTG 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
Db 131 TCGGAGTTGGAGGTGAAGAACCTATGTATCAAGCTCGGACGATCTTGTGGAGGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 191 AACGTGACGCGCGTCAAGTGCTCTGTCACGGTTTCGGGTGACATCATGCGCCAGTTTCA 250
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMet 80
Db 251 GATCTCATCGAGCTTTTCGCGATAGGAGGCAAGGCGGCCGACACCACTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
Db 311 GCGGACTATGAGATCGTGATATATTCTGTGAGACTGTGTGCTCTTAGTGCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
Db 371 AAGGTGCGGTATAGGATAGGATCAATCTTTGCGAGGGAACACGAGGAGGAGGAGT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
Db 431 ACGCAAGTATATGTTTCTATGATGAATGCTCGCGAAGTATGGAATGCGAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160

Db 491 AAGTACTTCACGGATCTGTTGCTGACTACTGCTGCTGACAGCTCTCATTTGA
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle
Db 551 TTTTGTCTTTCATGCTGCTGCTCTCCATCGCTCGACACATTAGATCATAT
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp
Db 611 GATCGTATTCAGGAAGTGCACGAGGCGCGATGTGTGATCTACTCTG
QY 201 AspAspArgCysGlyTyrGlyLysSerProArgGlyAlaGlyTyrThrPhe
Db 671 GATGATCTTGTGATGGGCAATTTCCACGAGAGGTGCGGTTATCTTT
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAla
Db 731 ATTGCAGAGCAGTTCATCATACCAATGGTCTAAGTTTGGTTGCACGTGC
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPhe
Db 791 CTGATGGGAAGGATACAAATTTGGTGCAGGATAAAAATGTTGTACACAGTTT
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly
Db 851 AATTACTGTATACCGCTGTGGGAACATGCGCCCATATGGAGATAGATGA
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal
Db 911 CGGTCTTTTCTCAGTTTCGAACACGACCGCGGCAAGTGAACCAAGATGT
QY 301 ThrProAspTyrPheLeu 306
Db 971 ACTCTGATTACTTTCTG 988
RESULT 2
ABX16239
ID ABX16239 standard; cDNA; 1365 BP.
XX AC ABX16239;
XX DT 08-APR-2003 (first entry)
XX DE P. patens protein phosphatase PP2A-4 cDNA.
XX Plant; ss; gene; PP2A-4; protein phosphatase; PHSRP; cold; i
KW phosphatase stress related protein; environmental stress; d
KW salt tolerance.
XX Physcomitrella patens.
FH Key Location/Qualifiers
CDS 71..991
FT /*tag= a
FT /product= "PP2A-4"
XX US2002152502-A1.
PN 17-OCT-2002.
XX 06-APR-2001; 2001US-00828302.
XX 07-APR-2000; 2000US-0196001P.
XX (SILV/) DA COSTA E SILVA O.
PA (BOHN/) BOHNERT H J.
PA (VTHI/) VAN THIELEN N.
PA (CHEN/) CHEN R.
PA (ISHI/) ISHITANI M.
XX Da Costa E SilvaO, Bohnert HJ, Van Thielen N, Chan R, I
XX WPI; 2003-198392/19.
XX P-PSDB; ABB74203.

XX New transgenic plant cell transformed by a Phosphatase Stress-Related
 PT Protein (PHSRP) coding nucleic acid, useful for modifying stress
 PT tolerance of a plant.
 XX
 PS Claim 18; Fig 2C; 79pp; English.
 XX
 CC The invention relates to a transgenic plant cell transformed by a
 CC Phosphatase Stress-Related Protein (PHSRP) coding nucleic acid. The
 CC expression of the nucleic acid in the plant cell results in increased
 CC tolerance to an environmental stress (e.g. salt tolerance, cold and
 CC drought) as compared to a wild type variety of the plant cell. Also
 CC include are a transgenic plant comprising the novel plant cell, a seed
 CC produced by the transgenic plant of (where the seed is true breeding for
 CC an increased tolerance to environmental stress as compared to a wild type
 CC variety of the plant cell, an agricultural product produced by the plant
 CC or seed, an isolated PHSRP or PHSRP coding nucleic acid, a recombinant
 CC expression vector comprising the nucleic acid, and producing a transgenic
 CC plant containing PHSRP nucleic acid. The transgenic protein (PHSRP) coding
 CC nucleic acid is useful for modifying stress tolerance of a plant. The
 CC present sequence encodes the PHSRP, protein phosphatase, PP2A-4
 XX
 SQ Sequence 1365 BP; 337 A; 282 C; 373 G; 373 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 9.72e-180 Length: 1365
 Score: 1670.00 Matches: 306
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-764-259-13 (1-306) x ABX16239 (1-1365)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
 DB 71 ATCGCTCATATGAGATGATAGACGGCAGATAGACGAGCTGCGAGTGCAAGCGGTG 130
 QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLysTrp 40
 DB 131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGAGACTGTGCTGTAGGAGAGTGG 190
 QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
 DB 191 AACGTGACGCGGTGAGTGTCTCTACGGTTTGGGTGACATCCATGCGCAGTTTCAAT 250
 QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrIleuPheMet 80
 DB 251 GATCTCATCGAGCTTTCCGCATAGGAGCAAGGCCCGCACCACTACTTTGTTTCATG 310
 QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerIleuLeuValAlaLeu 100
 DB 311 GCGGACTATGTGGATCGTGGATATTATTCTGTGCGAGACTGTGTGCTCTTAGTGGCCCTG 370
 QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIle 120
 DB 371 AAGTTCGGTATAGGATAGGATCAATCTTGGCAGGGAACCAACGAGGCGGCGAATT 430
 QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
 DB 431 ACGCAATATATGTTTCTATGATGAATGCTCGCGGAAGTATGGAATGCGAATGTTGG 490
 QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGluHisGluIle 160
 DB 491 AAGTACTTTCACGGATGTGTTCGACTACTCTGCTGACAGCTCTCATTTGAGCACGAGATT 550
 QY 161 PheCysLeuHisGlyLeuSerProSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
 DB 551 TTTTGTCTTCATGGTGGTCTGTCTCCATCGCTCGACATATTAGATCATCTCGAGCCCTA 610
 QY 181 AspArgIleGlnGluValProHisGlyGlyProMetCysAspLeuLeuTrpSerAspPro 200

DB 611 GATCGTATTCAAGAAGTCCCGCACGAGGGCCGAGTGTGTGATCTACTCTG CA 670
 QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh SP 220
 DB 671 GATGATCGTTGTGGATGGGCAATTTCCACGAGGTGCCGGTTATACTTT AT 730
 QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl EU 240
 DB 731 ATTGACAGAGCAGTTCAATCATACCAATGCTAAGTTTGGTTGCACGTGC TT 790
 QY 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPh RO 260
 DB 791 GTGATGGAAGGATACAAATTTGGTCCAGCATAAAAATTTGTGCACAGTTT CC 850
 QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGl SN 280
 DB 851 AATTACTGTTTACCGCTGTGGGAACATGCCGCCATAATGGAGATAGATGA AT 910
 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa YS 300
 DB 911 CGGTCCTTTCTCAGTTTCGATCGAACACGACCGCGGCAAAAGTGAACCAAGTGT AG 970
 QY 301 ThrProAspTyrPheLeu 306
 DB 971 ACTCTGATTACTTTCTG 988
 RESULT 3
 ACC43349
 ID ACC43349 standard; cDNA; 1386 BP.
 XX
 AC ACC43349;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Protein phosphatase stress-related polypeptide GmPP2A-5 CDN
 KW
 KW Protein phosphatase stress-related polypeptide; PPSRP; PpPF
 BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
 KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;
 XX drought; salinity; cold; enzyme; gene; ss.
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 CDS 92..1012
 FT /*tag= a
 FT /product= "protein phosphatase stress-relat
 FT polypeptide"
 XX
 PN W02003020914-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 05-SEP-2002; 2002WO-US028445.
 XX
 PR 05-SEP-2001; 2001US-0317305P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Bohnert HU, Chen R, Ishitani M, Van Thielien N, Da Costa O;
 FI WPI; 2003-300886/29.
 DR P-PSDB; ABP98034.
 XX
 PT New protein phosphatase stress-related polypeptide coding n
 PT useful for modulating plant's tolerance to an environmental
 PT as drought, increased salinity and cold.
 XX
 PS Claim 1; Page 82; 107pp; English.
 CC The present sequence encodes a protein phosphatase stress-r
 CC polypeptide (PPSRP). The specification describes PPSRP poly
 CC designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3,

CC GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived from
 CC Physcomitrella patens, Brassica napus, Glycine max or Oryza sativa. PPSRP
 CC polypeptides and polynucleotides are useful for modulating plant
 CC tolerance to an environmental stress such as drought or increased
 CC salinity and cold. They are also useful in identification and
 CC localization of Physcomitrella patens, Brassica napus, Glycine max or
 CC Oryza sativa and related organisms, mapping of genomes of organisms
 CC related to the above species, in a evolutionary and polypeptide
 CC structural studies, in determination of PPSRP regions required for
 CC function, modulation of PPSRP activity, modulation of metabolism of one
 CC or more cell functions and transmembrane transport of one or more
 CC components
 XX

SQ Sequence 1386 BP; 368 A; 273 C; 338 G; 407 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 5,95e-166 Length: 1386
 Score: 1549.00 Match: 280
 Percent Similarity: 96.73% Conservative: 16
 Best Local Similarity: 91.50% Mismatches: 10
 Query Match: 92.75% Indels: 0
 DB: 10 Gaps: 0

US-10-764-259-13 (1-306) x ACC43349 (1-1386)

Qy 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysIysPProLeu 20
 Db 92 ATGCCGTCTCAGCGGATCTGGAGGACAGATCGAGCAGCTGATGAGCTGCAAGCCTCTG 151
 Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLutrp 40
 Db 152 TCGGAGTCGGAGGTGAAGCGCTGTGGCAGTCAAGCGAGCGAGTCTTGTGGAGGATGG 211
 Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
 Db 212 AACGTGCAACCGTTAAGTGGCCCGTACCGTCTCGCGGATATTCACGGCCAGTTCTTAC 271
 Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrIleuPheMet 80
 Db 272 GATCTCATCGAGCTGTTTCGGATTGGAGGAAACGCTCCCGATACCAATATATCTCTTCATG 331
 Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
 Db 332 GGTGATTATGATGATCGTGATATTCATGATGAGAGCTGTTACACTTTTGGTGGCTTTG 391
 Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIle 120
 Db 392 AAAGTCCGTATAGAGATAGATACATCAATCTCAGGGGAATCATGAAGCGGTCAAT 451
 Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
 Db 452 ACTCAAGTGTATGGCTTCTATGATGAATGCTTGGAGAAATATGGAATCGCAATGCTCG 511
 Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
 Db 512 AAATACTTTACAGACTGTTGATTTATTTGCTCTGACTGCCCTCATTGAGAGTCAGATT 571
 Qy 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
 Db 572 TTCTGCTTGCATGAGGCTCTCTCACTCTTTTGGATACACTGGATAACATCAGAGCATTTG 631
 Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
 Db 632 GATCGTATTTCAAGAGGTTTCCATGAAGGACCAATGTGTGATCTCTTGTGGTCTGACCT 691
 Qy 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
 Db 692 GATGATCGCTGTGGATGGGATATCTTCACGTGTGTGAGGATACACATTTGGGCGAGAT 751
 Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
 Db 752 ATAGCTGCTCAGTTTAAATCATACCAATGCGCTCTCCCTGATATCGAGAGCACATCAGCTT 811

Qy 241 ValMetGluGlyTyrAsnTyrCysGlnAspIysAsnValValThrValPh 260
 Db 812 GTTATGGAAGGATTCATATTGGTGCAGGACAAAGATGTGGTACTGTATT 871
 Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGlu 280
 Db 872 AATTACTGTTATCGATGTGGGAATATGGCTGCCATCTACTAGAAATAGGAGA 931
 Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa 300
 Db 932 CAGAAATTTCTTCAGTTTGTATCCAGCTCCAGGCAAAATGTAGCCTGACAC 991
 Qy 301 ThrProAspTyrPheLeu 306
 Db 992 ACTCCAGATTATTTTGTG 1009

RESULT 4
 ACC43354
 ID ACC43354 standard; cDNA; 1330 BP.
 XX
 AC ACC43354;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Protein phosphatase stress-related polypeptide OsPP2A-5 cDN
 XX
 KW Protein phosphatase stress-related polypeptide; PPSRP; PpPP;
 KW BnPP2A-1; BnPP2A-2; BnPP2A-3; GmPP2A-1; GmPP2A-2; GmPP2A-3;
 KW OsPP2A-2; OsPP2A-3; plant tolerance; environmental stress;)
 XX drought; salinity; cold; enzyme; gene; ss.
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 FT CDS 104..1024
 FT /*tag= a
 FT /product= "protein phosphatase stress-relat
 FT polypeptide"
 XX
 PN WO2003020914-A2.
 XX
 PD 13-MAR-2003.
 XX
 PP 05-SEP-2002; 2002WO-US028445.
 XX
 PR 05-SEP-2001; 2001US-0317305P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Bohnert HJ, Chen R, Ishitani M, Van Thielens N, Da Costa
 XX
 DR WPI; 2003-300886/29.
 DR P-PSDB; ABP98039.
 XX
 PT New protein phosphatase stress-related polypeptide coding m
 PT useful for modulating plant's tolerance to an environmental
 PT as drought, increased salinity and cold.
 XX
 PS Claim 1; Page 87-88; 107pp; English.
 XX
 CC The present sequence encodes a protein phosphatase stress-r
 CC polypeptide (PPSRP). The specification describes PPSRP poly
 CC designated PpPP2A-1, PpPP-1, BnPP2A-1, BnPP2A-2, BnPP2A-3, (GmPP2A-2, GmPP2A-3, OsPP2A-1, OsPP2A-2 or OsPP2A-3, derived
 CC Physcomitrella patens, Brassica napus, Glycine max or Oryza
 CC polypeptides and polynucleotides are useful for modulating
 CC tolerance to an environmental stress such as drought or inc
 CC salinity and cold. They are also useful in identification a
 CC localization of Physcomitrella patens, Brassica napus, Glyc
 CC Oryza sativa and related organisms, mapping of genomes of o
 CC related to the above species, in a evolutionary and polypep
 CC structural studies, in determination of PPSRP regions requi
 CC function, modulation of PPSRP activity, modulation of metab

PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140821P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
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PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
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PR 19-JUL-1999; 99US-0144325P.
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PR 19-JUL-1999; 99US-0144332P.
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PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147933P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.

PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149417P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
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PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161359P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.: 3.99e-163
Score: 1522.00
Percent Similarity: 95.10%
Best Local Similarity: 89.54%
Query Match: 91.14%
DB: 3

Length: 921
Matches: 274
Conservative: 17
Mismatches: 15
Indels: 0
Gaps: 0

US-10-764-259-13 (1-306) x AAC43084 (1-921)

Db 270 AATGTTACGCGGTTAAGTGTCCGCTACCGCTGCGGCGACATCCACGGCAGTTTTCAC 329
Qy 61 AspleuileGluLeuPheArgileGlyLysAlaProAspThrAsnTyrLeuPheMet 80
Db 330 GATCTGATTGAGCTTTTAAAGATCGGTGTTCTTCGCTGACACCAATTAATCTCTTCATG 389
Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
Db 390 GGCAGATTACGTAGATCGAGGGTATTATTCTCTGGAGACAGTCTCGCTCTTGGTAGCACTC 449
Qy 101 LysValArgTyrArgAspArgIleThrileLeuArgGlyAsnHisGluSerArgGlnIle 120
Db 450 AAAGTTCGTACAGATAGGCTTACCATCTTAAGAGGGATACAGAAAGCGCCAAATTT 509
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
Db 510 ACTCAAGTGTATGGATTTTATGATGAGTGTCTAGAAAAATATGGAATATGCTAAATGCTCTGG 569
Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
Db 570 AAACACATTCACGTGACCTTTTGAATATCTCTTACAGCTCTCATCGAGATCAGGTT 629
Qy 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db 630 TTCGTGTTACATGGAGGCTCTCACCTTCTTTAGATACACTTGACACATCCGTTCTCTA 689
Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
Db 690 GATCGAATCCAAAGAGTTCCACATGAAGGACCTATGTGTGATCTGTTATGTCGATCCA 749
Qy 201 AspAspArgCysGlyTrpGlyLeuSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db 750 GATGATCATCGGTTGGGGAATATCTCTCTGTCGCGCAGGCTACACGTTTCGGAACAAGAT 809
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db 810 ATCGTACTCAGTTTAACACACCAATGAGCTCAGTCTGATCTCAAGAGCACACCACTT 869
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 870 GTCATGAAGGTTAATAATTTGGTGGCAAGAAAGACGTTGTGACTGTCTTTAGCGCCCA 929
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
Db 930 AACTATTCTCTACCGATGCGGCAACATGCTGCTATTCTAGAGATAGACGAAACATGGAC 989
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 990 CAGAACTTCTTTCAGTTTCAGTCCAGCCGCCACGTCAGTAGAACCAGCAACTACACGCANA 1049
Qy 301 ThrProAspTyrPheLeu 306
Db 1050 ACTCCAGATTACTTTTGG 1067
RESULT 7
ID ADX64434 standard; cDNA; 1732 BP.
XX
AC ADX64434;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 35277.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

OS Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
PF 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVU/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y.
PI WPI; 2004-180133/17.
DR New recombinant DNA construct, useful for improving plant to
PT cold, heat, drought, herbicides, extreme osmotic conditions
PT pests, for conferring increased resistance to plant disease
PT improving yield.
XX Claim 1; SEQ ID NO 35277; 15pp; English.
XX The invention describes a recombinant DNA construct compris-
CC polynucleotide consisting of a sequence encoding an amino a-
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The p-
CC of the invention are also useful in physical arrays of mole-
CC plant breeding markers. The recombinant DNA construct is us-
CC improving plant tolerance to cold, heat, drought, herbicides;
CC osmotic conditions, pathogens or pests, for manipulating gro-
CC plant cells by modification of the cell cycle pathway, for
CC increased resistance to plant disease, for producing galact-
CC lignin or plant growth regulators, for increasing the rate
CC recombination in plants, for improving yield by modification
CC photosynthesis or carbohydrate, nitrogen or phosphorus use,
CC or by providing improved plant growth and development under
CC stress condition or for modifying seed oil or protein yield
CC content. This sequence represents a plant full length inser-
CC polynucleotide that can be used in the recombinant DNA cons-
CC invention.
XX Sequence 1732 BP; 442 A; 392 C; 457 G; 441 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 2.75e-162 Length: 1732
Score: 1518.00 Matches: 272
Percent Similarity: 96.41% Conservative: 23
Best Local Similarity: 88.89% Mismatches: 11
Query Match: 90.90% Indels: 0
DB: 13 Gaps: 0
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Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal
Db 282 CCGAGGTGGAGGTTCAGACCTATGCGAGAGCAAGGCGATCCTCATY
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly
Db 342 AACGTACAGCCGCTGCGCTGCCCGTCACTGTGTGCGGCGACATCCACGG
Qy 61 AspleuileGluLeuPheArgileGlyGlyLysAlaProAspThrAsnTyr

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Db      402  |||||GACCTCATCGAGCTCTTCGCGATCGCGCGGCGCGCCAGACACCACTACCTCTTTATG 461
Qy      81  |||||GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
Db      462  GCGGATTAGCTGACCGTGGCTACTACTCTGTGGAGACTGTGTGTTGTAGTGGCTCTTA 521
Qy      101  LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
Db      522  AAGTACGTTATAGACAGACAGATCAATATTGAGAGGAAATCATGAGAGCAGACAAATA 581
Qy      121  ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyr 140
Db      582  ACTCAAGTGTATGGCTTCTATCATGAATCTTTCGCGAAATATCGAAATCGAAATGTGTGG 641
Qy      141  LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
Db      642  AAGTACTTTTACAGACTTGTGTATTTGATTTATTTTGGCTCTCACAGCTCTTATAGAAAACCATC 701
Qy      161  PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db      702  TTCTGCTACATGGTGGTCTCTCTCCATCACTGGATACATTGGATAATATCCGCGCCCTT 761
Qy      181  AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyrSerAspPro 200
Db      762  GATCGCATACAAGAGTCCCATCAAGGACCTATGTGTGATCTTTTGTGTCTGACCCA 821
Qy      201  AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db      822  GATGACCGATGTGGTGGGGAATTTCCACCAAGGGTGTGGGATACACATTTGGCCCAAGAT 881
Qy      221  IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db      882  ATTGCACAACAATTCAACCATCAAAATGGCTTAAGCTTATTTCAAGGGCACATCACTT 941
Qy      241  ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db      942  GTAATGAAGGCTTCAATTTGGTGTGAGGATAAGAATGTGTGACTGTGTTCAGCGCGCT 1001
Qy      261  AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
Db      1002  AACTACTGCTACCGATGCGGAACATGGCTGCAATCTCGAAATTTGGCGGAGAACATGGAT 1061
Qy      281  ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db      1062  CAGAACTTCTCCATTTGACCCAGCTCCACGGCAATTTGACCGGACATGACGCGCAAG 1121
Qy      301  ThrProAspTyrPheLeu 306
Db      1122  ACACCAAGACTACTTTTGT 1139
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ID AAC40149 standard; DNA; 1267 BP.
XX
AC AAC40149;
XX
XX 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27232.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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PR      29-MAR-1999; 99US-0126785P.
PR      01-APR-1999; 99US-0127462P.
PR      06-APR-1999; 99US-0128234P.
PR      08-APR-1999; 99US-0128714P.
PR      16-APR-1999; 99US-0129845P.
PR      19-APR-1999; 99US-0130077P.
PR      21-APR-1999; 99US-0130449P.
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PR      02-JUL-1999; 99US-0142055P.
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QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuLeuGluHisGluIle 160
Db 579 AAGTATTTTACGGACCTTTTCGATTATCTCCCTCTAAACAGCACTCATAGAGATCAGGTT 638
QY 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db 639 TTCTGTGTTGCATGGAGGCTTTTCACCTTCTCTGGATACTCTTGACAATATCCGAAGCTTG 698
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
Db 699 GATCGAATACAGAGGTTCCACAGAGGACCAATGTGGATCTACTCTGGTCTGATCCC 758
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db 759 GACGATCGTTGTGGATGGGAATATCTCTCGTGTGCTGGTTACACGTTTGCACAGGAC 818
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db 819 ATTGCTACTCAGTTCAATCAATCAATGAGCTGAGTCTGATATCAAGAGCGCATCAACTT 878
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 879 GTAATGAAGGCTAATATGGTGTGAGGAAAGACGTAGTACAGTGTATTAGTGACCA 938
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGluThrMetAsn 280
Db 939 AACTACTGTTACAGATGTGGAAACATGGCCGCAATCTTGAGATTGGAGAAAGATGGAA 998
QY 281 ArgSerPheLeuGlnPheGluProLalaProArgGlnSerGluProAspValThrArgLys 300
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XX ID AAC46572 standard; DNA; 1422 BP.
XX AC AAC46572;
XX DT 18-OCT-2000 (first entry)
XX ZE Zea mays DNA fragment SEQ ID NO: 50627.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic; pathway;
XX KW promoter; termination sequence; corn; ss.
XX OS Zea mays subsp. mays.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
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PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-015659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.

PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160814P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
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PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
Pred. No.: 2,21e-161 Length: 1422
Score: 1509.00 Matches: 269
Percent Similarity: 95.75% Conservative: 24
Best Local Similarity: 87.91% Mismatches: 13
Query Match: 90.36% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x AAC46572 (1-1422)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys; au 20
DB 217 ATGCCGTGCGACGGGGATCTGGACCGGAGATCGCGAGATCGCGGAGCTG 276
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal; p 40
DB 277 CCCGAGCGGAGGTCAGGGCGCTCTGCGAGCAGGCCAAGGCCATCCTTAT; g 336
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly; s 60
DB 337 AACGTGCAGCCGTGCGCTGTCTGTCAACCGTCTGTGGCGACATCCACGG; : 396
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy; t 80
DB 397 GACCTCATCGAGCTCTCCCGCATCGCGCGAGCGCTCCGACACCACTA; g 456
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu; u 100
DB 457 GCGGACTACGTCGATCGTGGCTACTATTCACTCGAAACAGTTTCTCTGTT; g 516
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe; e 120
DB 517 AAAGTCCGTTACAGAGATAGAATTACAATACTTAGAGGAAATCATGAGAG; c 576
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl; p 140
DB 577 ACTCAAGTATATGGCTTCTATGATGAATGCTTAGAAAAATATGGAATGCG; g 636
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGly; e 160
DB 637 AAGTATTTTACAGACTTGTGTTGATTTTGTGCTCTCTCACAGCTCTTATAGA; : 696
QY 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIle; u 180
DB 697 TTCTGTCTTCATGGTGGCTCTCTCCGTTCATTGGACACAGTTTCGATAATAT; t 756
QY 181 AspArgIleGlnGluValProHisGlyGlyProMetCysAspLeuLeuTrj; o 200
DB 757 GATCCGTACAGGAGGTTCCTCATGAAGGACCCATGTGTGATCTTTTGTG; a 816
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPh; p 220
DB 817 GATGACCGATGTGGATGGGAATTTTCAACAGAGAGGAGGAGGTTACACATT; c 876

PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
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PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
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PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:

Pred. No.: 1,578-161
Score: 1508.00
Percent Similarity: 94.44%
Best Local Similarity: 88.89%
Length: 921
Matches: 272
Conservative: 17
Mismatch: 17

Query Match: 90.30% Indels: 0
DB: 3 Gaps: 0
US-10-764-259-13 (1-306) x AAC43368 (1-921)
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCy eu 20
DB 1 ATCCGTTAAACCGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTC IA 60
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaAargThrIleLeuVa rp 40
DB 61 GGTGAAGCAGACGTGAAGATCCTTTGCCATCAAGCTAAAGCGATTCTTGT : : AT 120
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisG1 is 60
DB 121 AATGTTCAACCGTTAAGTGTCCGGTTACGGTATCGCGGATATCATGCG : : AT 180
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTy et 80
DB 181 GACCTAATTGAGCTATTTCGTATTGGTGGTAATGCTCCTGATACTAATTA TG 240
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeule eu 100
DB 241 GGAGATTATAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTATT : : TA 300
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe le 120
DB 301 AAGGTGCGTTACAGGACAGACTTACGATCTCGCAGGGAATCATGAGAG IT 360
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl rp 140
DB 361 ACACAAGTCTATGTTTATGACGAATGCTTGAGAAATACGGAATGCG GG 420
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleG1 le 160
DB 421 AAGTATTTCGAGACCTTTTCGATTATCTCCTCTTACAGCACTCATAGA : : IT 480
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI1 eu 180
DB 481 TTCTGTTTGCATGGAGGCTTTTACCTTCTCTGGATACTCTTGACAATAT TG 540
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr ro 200
DB 541 GATCGAATAAAGAGGTTCCACACGAGAGCAATGTGCGATCTACTCTG CC 600
QY 201 AspAspArgCysGlyTyrGlyLysSerProArgGlyAlaGlyTyrThrPh sp 220
DB 601 GACGATCGTTGTGGATGGGGAATATCTCCTCGTGTGCTGTACACGTI AC 660
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl eu 240
DB 661 ATTGCTACTAGTTTAAATCAACATGAGACTGAGTCTGATCTCAGAGC IT 720
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh ro 260
DB 721 GTAATGGAAGCTATAATTGGTGTGAGAAAGAACAGTAGTACAGTGTI CG 780
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspG1 sn 280
DB 781 AACTACTGTTTACAGATGGGAACATGGCCCAATTTCTTGAGATTGGAGA AA 840
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa ys 300
DB 841 CAGAACTTCTTCAATTCGATCCAGCACCTAGACAAAGTCGAAACCGGATAC AG 900
QY 301 ThrProAspTyrPheLeu 306
DB 901 ACCCTGATTATTTTGG 918

RESULT 12

ABZ12900
ID ABZ12900 standard; DNA; 921 BP.
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AC ABZ12900;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 705.
 XX
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200216655-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 24-AUG-2001; 2001WO-US026685.
 XX
 PR 24-AUG-2000; 2000US-0227866P.
 PR 26-JAN-2001; 2001US-0264647P.
 PR 22-JUN-2001; 2001US-0300111P.
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 PA (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Krops J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 PS Claim 144; SEQ ID NO 705; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 921 BP; 252 A; 183 C; 225 G; 261 T; 0 U; 0 Other;

Alignment Scores:
 Pred. NO.: 1.57e-161 Length: 921
 Score: 1508.00 Matches: 272
 Percent Similarity: 94.44% Conservative: 17
 Best Local Similarity: 88.89% Mismatches: 17
 Query Match: 90.30% Indels: 0
 DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x ABZ12900 (1-921)

QY 1 MetProserTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
 DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTGAAGCGGTTA 60
 QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
 DB 61 GGTGAAGCAGACGTCGAAGATCCTTTTCGATCAAGCTAAAGCGATTCTTGTTCGAGGAATAT 120
 QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlnPheHis 60
 DB 121 AATGTTCAACCCGTTAAGTGTCGGTACGGATCGCGGATATCCATGCGCCAGTTTAT 180
 QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
 DB 181 GACCTAATTGAGCTATTTCTGTTTGGTGTGTAATGCTCTCTGATACCTAAATTAACCTCTTCATG 240

QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
 DB 241 GGAGATTATGTAGATCGTGGCTACTATTCTGTGAGAAACAGTCTCTCTATT 300
 QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe: 120
 DB 301 AAGGTGCGTTACAGGACAGACTTACGATCTCTCGAGGGATCATGAGAG 360
 QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl: 140
 DB 361 ACACAAGTCTATGCTTTTATGACGAATGCTTGAAGAAATACGGAATGCG 420
 QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGln 160
 DB 421 AAGTATTTTACGGACCTTTTCGATTATCTCCTCTTACAGCACCCTATAGA 480
 QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 180
 DB 481 TTCTGTTTGCATGAGGCGCTTTCACCTTCTCTGGATACTCTTGACAATAT 540
 QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp 200
 DB 541 GATCGAATACAAAGAGTTCCACACGAAGACCAATGTGCGATCTACTCTG 600
 QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPhe 220
 DB 601 GACGATCGTGTGATGGGGAATATCTCTCTGCTGCTGCTGCTTACACGTT 660
 QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl: 240
 DB 661 ATTGCTACTCAGTTTAAATCATAAACATGGACTGAGTCTGATCTCAAGAGC 720
 QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPhe 260
 DB 721 GTAATGGAAGCTATATATTGGTGTGAGGAAAGAACGTAGTGACAGTCTT 780
 QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGln 280
 DB 781 AACTACTGTTACAGATGCGAAACATGCCCGCAATTCTTGAGATTGGAGA 840
 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa: 300
 DB 841 CAGAACTTCTTCAATTGATCCAGCAGCTAGACAAAGTCGAACCCGATAC 900
 QY 301 ThrProAspTyrPheLeu 306
 DB 901 ACCCGTGATTATTTTGG 918

RESULT 13
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 ID AAC44779 standard; DNA; 1344 BP.
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 AC AAC44779;
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 DT 18-OCT-2000 (first entry)
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 DE Zea mays DNA fragment SEQ ID NO: 44101.
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 KW Hybridisation assay; genetic mapping; gene expression contr
 KW protein identification; signal transduction pathway; metabo
 KW promoter; termination sequence; corn; ss.
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 OS Zea mays subsp. mays.
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 PN EP1033405-A2.
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 PD 06-SEP-2000.
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 PF 25-FEB-2000; 2000EP-00301439.
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 PR 16-SEP-1999; 99US-0154039P.
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Alignment Scores:

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Score: 1504.00 Matches: 269
Percent Similarity: 95.10% Conservative: 22
Best Local Similarity: 87.91% Mismatches: 15
Query Match: 90.06% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x AAC44779 (1-1344)

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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLutrp 40
DB 289 CCGAGGCGGAGGTCAAGGTGCTCTCGAGCAGGCCCAAGGCCATCTCTATGAGGAATGG 348
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 349 AACGTGACGCGTGGCTGCGTCCCGTACCGTCTCGCGGCAGCATCCACGGCCAGTCTAT 408
QY 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrIleuPheMet 80
DB 409 GACCTCATCGAGCTCTTCGCGATCGCGCGCACTCTCCGACCACTACCTCTCTCATG 468
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
DB 469 GCGGACTAGTCGTCGTGGCTATTATTCAGTTGAAACGGTTTCTCTGTAGTACTTGG 528
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIle 120
DB 529 AAAGTCGGTACAGAGATGAAATTAACAATCTTCGAGGAAATCATGAGAGCAGACAAATC 588
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QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
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DB 769 GATCGCATACAGGAGGTACCTCATGAAGGCCATGTGTGATCTTTTGTG 828
QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh 220
DB 829 GATGCCGATGTGGTGGGAATTTCAACCAGAGGAGCAGGTACACATT 888
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl 240
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RESULT 14

ABZ12766
ID ABZ12766 standard; DNA; 924 BP.
XX AC ABZ12766;
XX DT 21-JAN-2003 (first entry)
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 571.
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX OS Arabidopsis thaliana.
XX PN WO200216655-A2.
XX PD 28-FEB-2002.
XX PF 24-AUG-2001; 2001WO-US026685.
XX PR 24-AUG-2000; 2000US-0227866P.
XX PR 26-JAN-2001; 2001US-0264647P.
XX PR 22-JUN-2001; 2001US-0300111P.
XX PA (SCRI) SCRIPPS RES INST.
XX PI (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PI Harper JF, Krepes J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX PT Identifying a stress condition to which a plant cell has been producing plants with increased tolerance to these abiotic ;
XX PS Claim 144; SEQ ID NO 571; 577pp + Sequence Listing; English
XX CC The invention relates to identifying a stress condition to which a cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell array or probes representative of the plant cell genome; and

rg 281
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AG 846

hr 301
||
CT 906

DD 907 CCAGATTAATTTTTG 921

RESULT 15

BT 17-OCT-2000 (first entry)
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PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
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Alignment Scores:
Pred. No.:
Score:
Percent Similarity:

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95.41%
Length:
Matches:
Conservative: 23

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Best Local Similarity: 87.87%      Mismatches: 14
Query Match: 89.52%      Indels: 0
DB: 3      Gaps: 0

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DB 193 CGCGCGACCGGAGATATCGATCGTACAGATCGAGCAGCTTATCGAGTGTAAAGCGTTATCT 252
QY 22 GluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsn 41
DB 253 GAAACCGAGGTGAAGATGTGTGTGAGCAGCGAAAGACGATTCTTGTGGAAGAGTATAAT 312
QY 42 ValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHisasp 61
DB 313 GTTCAACCGGTTAAATGTCGGTTACCGTTCCTCTGCGGTGATATCCACGGCCAATTTTACGAT 372
QY 62 LeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMetGly 81
DB 373 CTAATCGAGCTTTTTCGTATCGGTGGTCTTCTCTGATACTAATTAATCTTTTCATGGGT 432
QY 82 AspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLys 101
DB 433 GATTATGTTGATCGAGGGTATTATTCTCTGGAGACAGTCTCACCTTTTGGTAGCACTGAAA 492
QY 102 ValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThr 121
DB 493 GTTTCGTACAGAGATAGACTTACTATCTCTAGAGGGAAATCATGAAAGCCGTCAAATTAAT 552
QY 122 GlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLys 141
DB 553 CAAGTGTATGGTTTATGATGAATGTTTGAGAAATATGGAATGCTAATGTATGGAG 612
QY 142 TyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePhe 161
DB 613 CACTTCACTGATCTTTTGGTATATCTTCCACTTACAGCTCTTATTGAGAGTCAGGTTTTC 672
QY 162 CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAsp 181
DB 673 TGTTTACATGAGGACCTTTCACCTCTTCTTAGATCACTTGACACATCCGATCTTTAGAT 732
QY 182 ArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAsp 201
DB 733 CGAATTCAAGAGGTTCCACATGAAGACCAATGTGTGATCTCTTATGCTGTATCCAGAT 792
QY 202 AspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIle 221
DB 793 GACCGATCGGTTGGGAAATATCTCTCGTGGTGAGGCTACACTTTCGGACAAGATATC 852
QY 222 AlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuVal 241
DB 853 GCTACTCAGTTTAAACCAACCAATGGACTCTCTCTGATTTCAAGAGCACATCAACTTGTTC 912
QY 242 MetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsn 261
DB 913 ATGGAAGGTTTTAATTTGGTCCAGAAAGAACCGTTGTGACTGTATTATTAGTGCCCAAC 972
QY 262 TyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArg 281
DB 973 TATTGCTACCGTTGTGGCAACATGCTCGGATTTAGAGATCGGTGAGAACATGACCCAG 1032
QY 282 SerPheLeuGlnProAlaProArgGlnSerGluProAspValThrArgLysThr 301
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QY 302 ProAspTyrPheLeu 306
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:25:12 ; Search time 3752 Seconds
(without alignments)
3815.791 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPROSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database :

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4: gb_hic:*
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8: gb_est7:*
9: gb_gss1:*
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11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1508	90.3	1429	4 AY104802 Zea mays
5	1493	89.4	1278	4 CNS0ADNP BX813410 Arabidops
6	1491	89.3	1250	4 CNS0ADL7 BX814752 Arabidops
7	1478	88.5	1534	4 AY108657 Zea mays

8	1428	85.5	1198	4 CNS0ADDDH BX816
9	1427	85.4	1749	4 CR594899 -leng
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11	1427	85.4	1781	4 CR596427 -leng
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18	1398	83.7	1016	5 BU901162 COURT
19	1393	83.4	1508	4 CNS0FWMV BU901
20	1393	83.4	1684	4 CNS0FSV6 aodon
21	1393	83.4	1770	4 CNS0FR02 aodon
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23	1391	83.3	923	1 AM011553 1533
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35	1368	81.9	1483	4 AY104329 stoso
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37	1366	81.8	1158	4 CNS0FLKE aodon
38	1365	81.7	1404	4 CNS0G531 aodon
39	1363	81.6	1538	4 CNS0FEZ8 aodon
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41	1359	81.4	870	5 BU133847 BUI33
42	1357	81.3	878	8 CAX14963 BX514
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				muscu

ALIGNMENTS

RESULT 1

CNS0ADRX 1283 bp mRNA linear
Arabidopsis thaliana Full-length cDNA Complete sequ
GSLT849ZD06 of Flowers and buds of strain col-0 of
thaliana (thale cress).

ACCESSION BX813946 GI:42474404

VERSION HTC; GSLT cDNA

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
rosids; eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 1283)

REFERENCE Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clef
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Scha
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat
Whole Genome Sequence Comparisons and 'Full-Length'
A Combined Approach to Evaluate and Improve Arabidop
Annotation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1283)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@ge
Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members
full-length libraries construction : Temple G.

EB-2004
Clone
sis

phyta;
edons;

uences:
me

ncage :
cns.fr

out

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES

Location/Qualifiers

source

1..1283

/organism="Arabidopsis thaliana"

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/gene="At1g10430"

gene

ORIGIN

Alignment Scores:

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Percent Similarity: 95.10% Conservative: 17
Best Local Similarity: 89.54% Mismatches: 15
Query Match: 91.14% Indels: 0
DB: 4 Gaps: 0

US-10-764-259-13 (1-306) x CNS0ADRX (1-1283)

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Db 176 ATGCGCTCGAAGGAGATCTGACCGTCAGATCGAGCTGATGAGTGTAAACCGTTA 235
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Qy 41 AenValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 296 AATGTTACGCGGTGAAGTGTCTGTACCGTTGCGGCGATTAATTCAGCGCCAGTTTAT 355
Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
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QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180  
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Db 1076 ACCCTGATTATCTTTTG 1093  
  
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DEFINITION cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL964875  
VERSION CL964875.1 GI:52384438  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 921)  
AUTHORS Ma L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang  
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H.,  
Wong, G.K.S., Deng, X.W. and Wang, J.  
TITLE An analysis of transcriptional regulation of the ric  
JOURNAL its comparison to Arabidopsis  
COMMENT Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
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Best Local Similarity: 87.91% Mismatches: 12  
Query Match: 90.54% Indels: 0  
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QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60  
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Db 361 ACCAAGTGTATGGCTTCATACGAATCTTACGGAAGTAGTGGAAATGCAAAATGTTGG 420
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
Db 421 AAGTACTTCACGGACTTGTTGATTATTGCTCTCTCACAGCTCTTTGTAGAAAACACAGTTC 480
QY 161 PheCysLeuHisGlyCysLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
Db 481 TTTTTCCTCCATGGCGGTCTCTCGCGCTCATTTGGATACATTGGATAAACATCGTGCCCTC 540
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
Db 541 GATCCATACAGAGGTCCCTCATGAGGCGCCATGTGTGATCTTTTGTGTCTGACCCG 600
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db 601 GACGATCGATGTGGTGGGAATTTCTCCAGAGGCGCAGGATACACGTTTGGGCAAGAT 660
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
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LOCUS AY104802
DEFINITION Zea mays PC0069597 mRNA sequence.
ACCESSION AY104802
VERSION AY104802.1 GI:21207880
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1429)
AUTHORS Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H.,
Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, F.,
Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
Jr.
Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
overgo hybridization
Plant Physiol. 134 (4), 1317-1326 (2004)
15020742
2 (bases 1 to 1429)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)

```

REFERENCE 3 (bases 1 to 1429)

AUTHORS Coe, E.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, Unive-
 Missouri, Columbia, MO 65211, USA
 COMMENT If you are interested in getting corresponding physi-
 cal clones, please contact the corresponding physi-
 cal clones are publicly available from ZmDB and may be found
 at www.zmdb.org; or NCB1, www.ncbi.nlm.nih.gov. When the
 maize cDNA sequences are either Virginia Walbot, Stan-
 Schnable, Iowa State, then clones may be requested from
www.zmdb.iastate.edu.

FEATURES

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 Mapping Project"

ORIGIN

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 Score: 1508.00 Matches: 272
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 Best Local Similarity: 88.60% Mismatches: 11
 Query Match: 90.30% Indels: 1
 DB: 4 Gaps: 0
 US-10-764-259-13 (1-306) x AY104802 (1-1429)

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QY 41 AsnVal-GlnProValLysCysProValThrValCysGlyAspIleHisG:
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LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTFB162A06 of Flowers and buds of strain col-0 of Arabidopsis
SOURCE thaliana (thale cress).
BX813410
ACCESSION BX813410.1 GI:42473857
VERSION HTC; GSLT cDNA.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1278)
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1278)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Location/Qualifiers
1. 1278
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FEATURES
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ORIGIN

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Best Local Similarity: 88.24% Mismatches: 17
Query Match: 89.40% Indels: 0
Gaps: 4
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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaAraGThrIleLeuVa rp 40
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QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGl : :
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Db 777 GATGATCGATGGATGGGGAATATCTCCACAGAGGTGCTGGTTATACAT : :
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl eu 240
Db 837 ATCGCAGCTCAATTAATAACAACTAAGTCTCATATCAAGAGC : :
QY 241 ValMetGluGlyTyrAsnThrCysGlnAspLysAsnValThrValPh ro 260
Db 897 GTCATGGAAGGTTTAACTGTGTGAGATTAAGATGTGGTTACTGTGTI CA 956
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGl sn 280

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Db      957 AACATTGCTACCGGTGGGAACATGCTGCTTCTAGAGATAGGAGATACATGGAG 1016
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Qy      281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
      :::::
Db      1017 CAAAACTTCCTCCAGTTCGATCCAGCTCTCTGACAAAGTTGAACCTGATACTACTCGGAAG 1076
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Qy      301 ThrProAspTyrPheLeu 306
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Db      1077 ACCCTGATTGTGCTTG 1094

RESULT 6
CNSOADL7
LOCUS
DEFINITION
  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
  thaliana (thale cress).
ACCESSION
  BX814752
VERSION
  BX814752.1 GI:42474221
KEYWORDS
  HTG; GSLT cDNA.
SOURCE
  Arabidopsis thaliana
  Arabidopsis thaliana
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicaceae; Arabidopsi.
REFERENCE
  1 (bases 1 to 1250)
  Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
  Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
  Temple,G., Caboche,M., Weissenbach,J. and Salanoubat M.
  Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
  A Combined Approach to Evaluate and Improve Arabidopsis Genome
  Annotation
JOURNAL
  Unpublished
REFERENCE
  2 (bases 1 to 1250)
  Genoscope.
AUTHORS
  Direct Submission
TITLE
  Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  - Web : www.genoscope.cns.fr)
COMMENT
  The sequences are based on single pass reads.
  Life Technologies (a division of Invitrogen) members carried out
  full-length libraries construction : Temple G.
  Genoscope members carried out sequencing and annotation : Castelli
  V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
  Schachter V., Weissenbach J., Salanoubat M.
  URV INRA : Clepet C., Caboche M.
  Annotation is based on the June 2003 version of the Arabidopsis
  genome released by MIPS (Munich Information center for Protein
  Sequences). 5 prime and 3 prime are assembled with Phrap.
  http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
  length
  http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES
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      /clone="GSLTFB92E04"
      /tissue_type="flowers and buds"
      /ecotype="Col-0"
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      complement(1..1250)
      /gene="At1G59830"

ORIGIN
  Alignment Scores:
  Pred. No.:      6,67e-163      Length:      1250
  Score:          1491.00      Matches:      270
  Percent Similarity: 93.79%      Conservative: 17
  Best Local Similarity: 89.24%      Mismatches: 19
  Query Match:      0          Indels:      0
  DB:              4          Gaps:      0

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    complement(1..1250)
    /gene="At1G59830"

ORIGIN
  RESULT 7
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  LOCUS
  DEFINITION
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  ACCESSION
    AY108657
  VERSION
    AY108657.1 GI:21211829
  KEYWORDS
    HTC.

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US-10-764-259-13 (1-306) x CNSOADL7 (1-1250)
Qy      1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys:
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Db      181 ATGCCGTTAAACCGAGATCTCGACCGTCAGATCGAACAGCTAAATGGAGTT
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Qy      21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal:
      |||
Db      241 GGTGAAGCAGACGCTGAAGATCTCTTTGGCATCAAGCTAAAGCGATTCTTGT
      |||
Qy      41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly:
      |||
Db      301 AATGTTCAACCGTTAAGTGTCCGTTACGGTATGCCGGCATATCCATGG:
      |||
Qy      61 AspLeuIleGluLeuPheAtrGileGlyGlyLysAlaProAspThrAsnTy:
      |||
Db      361 GACCTAATGAGCTATTTTCGTATTGGTGAATGCTCTCTGATATAATTA
      |||
Qy      81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe:
      |||
Db      421 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAAACAGTCTCTCTATT
      |||
Qy      101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe:
      |||
Db      481 AAGTGGGTTACAGGACAGACTTACGATCTCTGCGAGGAATCATGAGAG:
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Qy      121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl:
      |||
Db      541 ACACAAGTCTATGTTTTTATGACGAATGCTTTGAGGAAATACGGAAATGCT:
      |||
Qy      141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGly:
      |||
Db      601 AAGTATTTTACGGACCTTTTCGATTATCTCCTCTTACAGCACTCATAG:
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Qy      161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIl:
      |||
Db      661 TTCGTGTTGCAAGGAGGCTTTTCACTCTCTGATCTCTTGACCAATAT:
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Qy      181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr:
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Db      721 GATCGAATACAAGAGGTTCCACACAGGACCAATGTCGATCTACTCTG:
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Qy      201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh:
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Db      781 GACGATCGTTGTGATGGGGAATATCTCTCTGCTGCTGTGTACACGTT
      |||
Qy      221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaAtqAl:
      |||
Db      841 ATTGCTACTCAGTTTAATCATACATGGAATGAGTCTGATCTCAAGAGCT:
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Qy      241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh:
      |||
Db      901 GTAATGAAGCTATATAATTGGTGTGAGGAAAGAACGTTAGTGACAGTGT:
      |||
Qy      261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly:
      |||
Db      961 AACTACTGTTACAGATGTGGAACAATGCGCCCAATTTCTTGAGATTGGAGA:
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Qy      281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal:
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Db      1021 CAGAACTTCTTCAATTCGATCCAGCACTTAGACAAAGTCGAACCCGATAC:
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Qy      301 ThrProAspTyrPheLeu 306
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Db      1081 ACCCTGATTATCTTTTG 1098

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SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS 1 (bases 1 to 1534)
Gardiner, J., Schroeder, S., Polacco, M.L., Sanchez-Villeda, H., Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, P., Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H. Jr.

TITLE Anchoring 9,371 maize expressed sequence tagged unigenes to the bacterial artificial chromosome contig map by two-dimensional overgo hybridization
JOURNAL Plant Physiol. 134 (4), 1317-1326 (2004)
PUBMED 15020742
REFERENCE 2 (bases 1 to 1534)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
AUTHORS Zea Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 3 (bases 1 to 1534)
Coe, E.H.
AUTHORS Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
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1..1534
/organism="Zea mays"
/mol_type="mRNA"
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/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN
Alignment Scores:
Pred. No.: 2,94e-161 Length: 1534
Score: 1478.00 Matches: 268
Percent Similarity: 94.81% Conservative: 24
Best Local Similarity: 87.01% Mismatches: 14
Query Match: 88.50% Indels: 2
DB: 4 Gaps: 0

US-10-764-259-13 (1-306) x AY108657 (1-1534)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
DB 192 ATGCGGTGCGACGGGATCTGGACCGGACGATCGCGAGTCGCGAGTCTGCAAGTACCTG 251
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLtrp 40
DB 252 CCCGAGGGGGAGGTCAAGCGCTCTCGAGCAGGCGCAAGCCATCTTATGGAGGAGTGG 311
QY 41 AnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 312 AACGTGACGCCGTGCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGT 371
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnThrLeuPheMet 80

DB 372 GACCTCATCGAGCTCTTCCGCATCGCGGCGACTCTCCCGACACCAACTA
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe
DB 432 GCGCAGCTACGTCGATCGTGGCTATTATTACGTTGAAACAGATTCTCTGT
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe
DB 492 AAAGTCGTTACAGATAGAAATTAACAATACTTAGAGGAAATCATGAGAG
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl
DB 552 ACTCAAGTATATGCTCTCTATGATCAATGCTTAAGAAAAATATGGAATGC
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuLeG1
DB 612 AAGTATTTTACAGACTTGTGTTGATTTTGTGCTCTCACAGCTCTTATAGA
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI1
DB 672 TTCTGTCTTCATGCTGGCTCTCTCCGTCAATTGGACACATTGGATAATAT
QY 181 AspArgIleGlnGluValPro-HisGluGlyProMetCysAspLeuLeu1
DB 732 GATCGCGTACAGGAGTTCCTCCATGAAGGACCCATGTGTGATCTTTGT
QY 200 oAspAspArgCysGlyTrpGlyIleSerProArgGlyValaGlyTyrThrF
DB 792 AGATGACCGATGTGGATGGGGAATTTACCAAGAGGACGAGTTACACAT
QY 220 pIleAlaGlnPheAsnHisThrAsnGlyLeuSerLeuValaAlaArgA
DB 852 CATTGGCAGCAGTTCACCATACAAATGGTCTTTCTCTCATTTCAAGGG
QY 240 uValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValF
DB 912 TGTAAATGGAGGATTTAATTTGGTGGCCAGGATAAGAAATGTAGTCACAGTC1
QY 260 oAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspG
DB 972 TAATTACTGTTTACCCTGTGTGTAACATGCTGCTATCTTGAATTCGGGG
QY 280 nArgSerPheLeuGlnPheGluProAlaProArg-GlnSerGluProAsf
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QY 300 ysThrProAspTyrPheLeu 306
DB 1092 AAACCCAGAGTACTTTCTG 1111

RESULT 8
CNS0ADDH 1198 bp mRNA linear
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequ
DEFINITION GSLTPGH57ZF10 of Hormone Treated Callus of strain cc
ACCESSION Arabidopsis thaliana (thale cress).
VERSION BX816593.1 GI:42474290
KEYWORDS HTC; GSLT_cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
AUTHORS rosid; eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 1198)
Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clef
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Scha
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat
Whole Genome Sequence Comparisons and 'Full-length'
A Combined Approach to Evaluate and Improve Arabidof
Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1198)


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Db 467 AGAGGATATATTCAGTTGAACAGGTACACTGCTGTAGCTCTTAAGTTCGTACCGT 526
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly 125
Db 527 GAACGCATCACCATTCTTCGAGGGAATCATGAGAGCAGACAGATCACACAAGTTTATGGT 586
QY 126 PheTyrAspGluCysLeuArgIleTyrGlyAsnAlaAsnValTyrPheThrAsp 145
Db 587 TTCTATGATGAATGTTTAAGAAATATGGAATGCAAAATGTTTGAATAATTTTACAGAT 646
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165
Db 647 CTTTGTGACTATCTTCCTCTCACTGCCTTGGTGGATGGCAGATCTTCGTCTACATGGT 706
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu 185
Db 707 GGTCTCTCGCCATCTATAGATACACTGGATCATATCAGAGCAGCTTGTATCGCTACAAGAA 766
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAspArgCysGly 205
Db 767 GTTCCCATGAGGGTCCCAATGTGTGACTTGTGCTGGTCCAGATCCAGATGACCGTGGTGGT 826
QY 206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe 225
Db 827 TGGGGTATATCTCTCTCGAGAGCTGGTTACACTCTTTGGCAAGATATTTCTGAGACATTT 886
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
Db 887 AATCATGCCAATGGCTCAGCTTGGTGTCTAGAGCTCACCAGCTAGTGTATGGAGGATAT 946
QY 246 AsnTyrCysGlnAspIleAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db 947 AACTGTGTGCATGACGGGAATAGTAGTAACGATTTTCAGTGTCTCCAAACTATTGTATCGT 1006
QY 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285
Db 1007 TGTGGTAACAGCTGCAATCATGAGCACTTGACGATACTCTAAATACTCTTTCTTGAG 1066
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
Db 1067 TTTGACCCAGCACTCGTAGAGCGAGCCACATGTTACTCGTCTGACCCAGACTACTTC 1126
QY 306 Leu 306
Db 1127 CTG 1129
RESULT 11
LOCUS CR596427
DEFINITION full-length cDNA clone CS0DE009YC05 of Placenta of Homo sapiens
(human).
ACCESSION CR596427
VERSION CR596427.1 GI:50477234
KEYWORDS HTC; CRLST_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1781)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1781)
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) pri
end enriched, double-strand cDNA was digested with N
into the Not I and EcoR V sites of the pCMVSPORT 6 v
was normalized. Library was constructed by Life Tech
division of Invitrogen.

FEATURES
Location/Qualifiers
source 1..1781

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="CS0DE009YC05"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 3,32e-155 Length: 1781
Score: 1427.00 Matches: 252
Percent Similarity: 94.35% Conservative: 32
Best Local Similarity: 83.72% Mismatches: 17
Query Match: 85.45% Indels: 0
DB: 4 Gaps: 0

US-10-764-259-13 (1-306) x CR596427 (1-1781)

QY 6 AspValAspArgGlnIleGluGlnSerGluCysLysProLeuSerGln 25
Db 202 GAGCTGGACCACTGGATCGAGCAGCTGAACAGTGCAGAGCTGTCCGA 261
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTyrAsnVa 45
Db 262 AAGAGCTCTCGAGAGAGGCTAAAGAAATCTGACAAAAGAAATCCACG 321
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLe 65
Db 322 CGATGTCAGTTACTGTCTGTGGAGATGTCATGGCAATTTTCATGATCT 381
QY 66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAs 85
Db 382 TTTAGAATTGGTGGCAAAATCACCAGATACAAATTTACTTGTATTGGGAGA 441
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa 105
Db 442 AGAGGATATTATTAGTTGAACAGTGTACACTGCTGTAGCTCTTAAGGT 501
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlu 125
Db 502 GAACGCATCACCATTCTTCGAGGGAATCATGAGAGCAGACAGATCACACA 561
QY 126 PheTyrAspGluCysLeuArgLysThrGlyAsnAlaAsnValTyrLysTy 145
Db 562 TTCTATGATGAATGTTTAAGAAATATGGAATGCAAAATGTTTGGAAATA 621
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCy 165
Db 622 CTTTGTGACTATCTCTCTCACTGCCTTGGTGGATGGGAGATCTTCTG 681
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr 185
Db 682 GGTCTCTCGCCATCTATAGATACACTGGATCATATCAGAGCAGCTTGATCG 741
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAs 205
Db 742 GTTCCCATGAGGGTCCCAATGTGTGACTTGTGCTGGTCCAGATCCAGATGA 801
QY 206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl 225
Db 802 TGGGGTATATCTCTCGAGAGGCTGGTTTACACCTTTTGGGCAAGATATTTC 861
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe 245
Db 862 AATCATGCCAATGSCCTCACGCTGCTGTGTCTAGAGCTCACCAGCTAGTGAT 921

: prime
cloned
brary
a

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QY 246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db 922 AACTGGTGCATGACCGAATAGTAGAAGATTTTCAGTGTCTCCAAACTATTGTATCGT 981
QY 266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
Db 982 TGTGTAAACCAAGCTGCAATATGGAACCTTGACGATACTCTAAAATACTCTTTCTTGCG 1041
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
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QY 306 Leu 306
Db 1102 CTG 1104

RESULT 12
LOCUS CR619537
DEFINITION CR619537 1830 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CSODM014YH02 of Fetal liver of Homo sapiens
(human).
ACCESSION CR619537
VERSION CR619537.1 GI:50500344
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1830)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1830)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1830
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ORIGIN
Alignment Scores:
Pred. No.: 3,45e-155 Length: 1830
Score: 1427.00 Matches: 252
Percent Similarity: 94.35% Conservative: 32
Best Local Similarity: 83.72% Mismatches: 17
Query Match: 85.45% Indels: 0
DB: 4 Gaps: 0

US-10-764-259-13 (1-306) x CR619537 (1-1830)

QY 6 AspValAspArgGlnIleGluLeuSerGluCysLysProLeuSerGluLeuGluVal 25
Db 253 GAGCTGGACCACTGATCGACAGCTGACAGTGCAGAGCTGTCCGAGTCCAGCTC 312
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluThrAsnValGlnProVal 45

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Db 313 AAGACCTCTCGAGAGCGCTAAAGAAATCCTGCACAAAGAAATCCACCGT
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Db 373 CGATGTCCAGTTACTGTCTGTGGAGATGTCATGGGCAATTTTCATGATCT
QY 66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAs
Db 433 TTTAGAAATTTGGTGGCAATCACCAGATACAAATTAATTCTTTATGGGAGA
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa
Db 493 AGAGGATATTATTAGTTGAAACACAGTTACACTGCTTGTAGCTCTTAAGGT
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGl
Db 553 GAACGCATCAACCATTTCTTCGAGGGAATCATGAGAGCAGACAGATCACACA
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyrLysTy
Db 613 TTCTATGATGATGTTTAAAGAAATATGGAATGCAATGTTTGGAAATP
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuLeuGluHisGluIlePheCy
Db 673 CTTTGTGACTATCTCTCTCACTGCTTGGTGGATGGCAGATCTTCTG
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr
Db 733 GGTCTCTCGCCATCTATAGATACACTGGATCATATCAGAGCACTTGTATCG
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAs
Db 793 GTTCCCATGAGGCTCCATGTGTGACTTGTGTGTGTCAGATCCAGATGA
QY 206 TrpGlyLeuSerProArgGlyAlaIleGlyTyrThrPheGlyGlnAspIleAl
Db 853 TGGGTATATCTCTCGAGAGCTGGTTACACCTTTGGGCAAGATATTTC
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValme
Db 913 AATCATGCCAATGGCTCACTGCTGTGTAGAGCTCACCAGCTAGTGTAT
QY 246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTy
Db 973 AACTGTGTGCCATGACCGGAATGTAGTAACGATTTTCAGTGTCCAAACTP
QY 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe
Db 1033 TGTGTAACCAAGCTGCAATCATGGAACCTTGACGATCTCTAAAATACTC
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPi
Db 1093 TTTGACCCAGCACCTCGTAGAGCGGAGCCACATGTTACTCTGTCGTACCCC
QY 306 Leu 306
Db 1153 CTG 1155

RESULT 13
LOCUS AK076110
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIK
enriched library, clone:2810407123 product:protein F
catalytic subunit, alpha isoform, full insert sequen
AK076110
ACCESSION AK076110.1 GI:26345081
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1

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tomi;

PR-2004
length
se 2a,


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Db      911 AATCATGCCAATGGCCTCAGCTTGCTGTCAGAGCTCACCAGCTGGTGATGGAGGGATAT 970
Qy      246 AsnTTPCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db      971 AACTGGTCCCATGACCGGAAGCTAGTAAATTTTCAGTGTCTCCAAATATTGCTATCGT 1030
Qy      266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
Db      1031 TGTGTGAACCAAGCTGCAATCATGGAACCTTGACGACACTCTTAAAGTATTCTTCTTGCAG 1090
Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
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Qy      306 Leu 306
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RESULT 14
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LOCUS      1983 bp      mRNA      linear      HTC 31-JAN-2005
DEFINITION      Sus scrofa clone Clu_2818.scr.msk.pl.Contig3, mRNA sequence.
ACCESSION      AY609733
VERSION      AY609733.1 GI:52351301
KEYWORDS      HTC.
SOURCE      Sus scrofa (pig)
ORGANISM      Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE      1 (bases 1 to 1983)
AUTHORS      Jorgensen,F.G., Hobolth,A., Hornshoj,H., Bendixen,C., Fredholm,M.
            and Schierup,M.H.
TITLE      Comparative analysis of protein coding sequences from human, mouse
            and the domesticated pig
JOURNAL      (er) BMC Biol. 3 (1), 2 (2005)
PUBMED      15679890
REFERENCE      2 (bases 1 to 1983)
AUTHORS      Hornshoj,H., Bendixen,C. and Panitz,F.
TITLE      Direct Submission
JOURNAL      Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
            Institute of Agricultural Sciences, Research Centre Foulum, Postbox
            50, Tjele DK-8830, Denmark
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            Location/Qualifiers
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            /db_xref="taxon:9823"
            /clone="Clu_2818.scr.msk.pl.Contig3"
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            /note="similar to M20192.1 Porcine protein phosphatase 2A
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ORIGIN

Alignment Scores:
Pred. No.:      3.86e-155      Length:      1983
Score:      1427.00      Matches:      252
Percent Similarity:      94.35%      Conservative:      32
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US-10-764-259-13 (1-306) x AY609733 (1-1983)

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Qy      26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluThrAsnValGlnProVal 45
Db      314 AAGACCTCTCGGAGGCTTAAGAAATCTCTGACAAAGAAATCCAACTGCAAGAGGTT 373
Qy      46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65

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Qy      66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAs 85
Db      434 TTTAGAATTGGTGCAAAATCACCAGATACGAAATTTACCTGTTTATGGGAGA 493
Qy      86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVa 105
Db      494 AGAGGATATTATTCCGTTGAAACAGTTACTCTGCTGTAGCTCTTAAGGT 553
Qy      106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGl 125
Db      554 GAACGCATCACCATCTTCGAGGAAATCATGAGAGCAGACAGATCACACA 613
Qy      126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTropLysTy 145
Db      614 TTCTATGATGAGTGTTTAAGGAAATATGGAATGCAATGTTTGGAAAT 673
Qy      146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCy 165
Db      674 CTTTTTGATTATCTCTCTCCTCATTGATAGTGGATGGGAGATCTTCTG 733
Qy      166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr 185
Db      734 GGCCTCTCACCATCCATAGATACACTGATGCATCAGAGCACCTTGATCG 793
Qy      186 ValProHisGluGlyProMetCysAspLeuLeuTyrPseAspProAspAs 205
Db      794 GTTCCCATGAGGGTCCCAATGTGTGACTGTGCTGGTCAGATCCAGATGA 853
Qy      206 TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAl 225
Db      854 TGGGGTATATCTCTCCAGAGAGCTGGTTACACTTTTGGGCAAGATATTTC 913
Qy      226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe 245
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Qy      246 AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTy 265
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Qy      266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe 285
Db      1034 TGTGGGAACCAAGCTGCAATCATGGAACCTTGATGATCTCTAAATACTC 1093
Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 305
Db      1094 TTTGACCCAGCACCTCGCAGAGGGGAGCCACACGTTACTCGCTGACCCC 1153
Qy      306 Leu 306
Db      1154 CTG 1156

RESULT 15
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LOCUS      1274 bp      mRNA      linear
DEFINITION      Arabidopsis thaliana Full-length cDNA Complete sequ
            GSLTPGH222A06 of Hormone Treated Callus of strain cc
            Arabidopsis thaliana (thale cress).
ACCESSION      BX816000
VERSION      BX816000.1 GI:42473421
KEYWORDS      HTC; GSLT cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core e
            rosid; eurosoids II; Brassicales; Brassicaceae; Arab
            1 (bases 1 to 1274)
            Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clef
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Scha
            Temple,G., Caboche,M., Weissensbach,J. and Salanoubat

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GenCore version 5.1.6
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Run on: December 9, 2005, 10:27:22 ; Search time 203 Seconds
(without alignments)
2679.477 Million cell updates/sec

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Fgapop 6.0, Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	ID	Description
1	1670	100.0	1365	US-09-828-302-8
2	1427	85.4	1787	Sequence 39, Appl
3	1427	85.4	2181	Sequence 17, Appl
4	1427	85.4	2182	Sequence 5543, Ap
5	1427	85.4	2966	Sequence 3, Appl
6	1411	84.5	1522	Sequence 5464, Ap
7	1411	84.5	1541	Sequence 590, Appl
8	1411	84.5	1781	Sequence 10, Appl
9	1411	84.5	1843	Sequence 10, Appl

10	1411	84.5	2574	3	US-09-780-045-3	Sequ
11	1366	81.8	1721	3	US-09-190-976B-11	Sequ
12	1291	77.3	1134	3	US-09-487-558B-269	Sequ
13	1286	77.0	1110	3	US-09-614-221A-47	Sequ
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15	1137.5	68.1	1339	3	US-09-949-016-2909	Sequ
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20	963.5	57.7	957	3	US-09-248-796A-4207	Sequ
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23	786	47.1	816	3	US-09-248-796A-4206	Sequ
24	757	45.3	2263	3	US-09-825-497A-42	Sequ
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31	701	42.0	459	3	US-09-300-958A-38	Sequ
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ALIGNMENTS

RESULT 1
US-09-828-302-8
; Sequence 8, Application US/09828302
; Patent No. 6818805
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-8

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Score:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
US-10-764-259-13 (1-306) x US-09-828-302-8 (1-1365)			


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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
Db 131 TCGGAGTTGGAGGTGAAGAACTATGTGATCAAGCTCGACGATCTTGGTGAGGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 191 AAGGTGACGCGGTGAGTGTCTGTACGGTTTCGGGTGACATCCATGGCCAGTTTCAT 250
QY 61 AspleuIleGluLeuPheArgIleGlyCysAlaProAspThrAsnTyrIleuPheMet 80
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QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
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QY 301 ThrProAspTyrPheLeu 306
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RESULT 2

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US-09-300-958A-39
; Sequence 39, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McCelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
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; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets ;
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 1787
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-300-958A-39

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Best Local Similarity: 83.72% Mismatches: 17
Query Match: 85.45% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-300-958A-39 (1-1787)

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QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeu 1 65
Db 327 CGATGTCAGTTACTGTCTGTGGAGATGTGCATGGCAATTTTCATGATCT 1 386
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QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlu 1 125
Db 507 GAACGCAATCACCATTTCTTCGAGGGAATCATGAGAGCAGACAGATCCACA 1 566
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyr 1 145
Db 567 TTTCTATGATGAATGTTTAAAGAAAATATGGAATGCAATGTTTGGAAATA 1 626
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCys 1 165
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Db 927 AACTGGTCCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAAACTATTGTATCGT 986
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QY 306 Leu 306
Db 1107 CTG 1109
RESULT 3
US-09-780-049-17
; Sequence 17, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 17
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (210)...(1139)
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Alignment Scores:
Pred. No.: 6,17e-172 Length: 2181
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US-10-764-259-13 (1-306) x US-09-780-049-17 (1-2181)
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Db 234 GAGCTGGACCACTGGATCGAGCAGCTGAACAGCTGCAAGCAGCTGTCCGAGTCCAGGTC 293
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluThrAsnValGlnProVal 45
Db 294 AAGACCTCTCGGAGGCTTAAGAAATCTTCACAAAGAAATCAACAGTCAAGAGGTT 353
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65
Db 354 CGATGTCCAGTTACTGTCTGTGGAGATGTGCATGGCGCAATTCATGATCTCATGGAATG 413
QY 66 PheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
Db 414 TTTAGAATTGGTGGCAAAATCACCAGATCAAAATTAATCTGTTTATGGAGATTAATGTTGAC 473
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeuLysValArgTyrArg 105
Db 474 AGAGGATATTATTAGTTGAACAGTGTACACTGCTTTGAGCTCTTAAGGTTGTTACCGT 533
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly 125
```

```
Db 534 GACGCGCATCACTTCCTCGAGGGAATCATCGAGAGCAGACAGATCACACA
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyr
Db 594 TTTCTATGATGAATGTTTAAGAAATATGGAATGCAAAATGTTTGGAAAT
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCys
Db 654 CTTTTTGACTATCTCTCTCCTCCTCCTGCTGGTGGATGGGAGATCTTCTG
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArg
Db 714 GGTCTCTCGCCATCTATAGATACACTGCGATCATATCAGAGCACTTGTATCG
QY 186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAs
Db 774 GTTCCCATGAGGGTCCAATGTGTGACTTGTCTGGTGCAGATCCAGATGA
QY 206 TrpGlyIleSerProArgGlyValAlaGlyTyrThrPheGlyGlnAspIleAla
Db 834 TGGGGTATATCTCTCGAGGAGCTGTTACACCTTTGGGCAAGATATTTTC
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMet
Db 894 AATCATGCCAATGGCTCACCCTGCTGTGTAGAGCTCACCAGCTAGTGTAT
QY 246 AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyr
Db 954 AACTGGTGGCCATGACCGGAATGTAGTAACGATTTTCAGTGTCTCCAAACTA
QY 266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSer
Db 1014 TGTGTAAACCAAGCTGCAATCATCGAACTTGACGATCTCTAAAATACTC
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPyr
Db 1074 TTTGACCCAGCACCTCGTAGAGCGGAGCCACATGTTACTCGTCTGATCCCC
QY 306 Leu 306
Db 1134 CTG 1136
RESULT 4
US-09-949-016-5543
; Sequence 5543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5543
; LENGTH: 2182
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5543
Alignment Scores:
Pred. No.: 6,17e-172 Length: 2182
Score: 1427.00 Matches: 252
Percent Similarity: 94.35% Conservative: 32
Best Local Similarity: 83.72% Mismatches: 17
```

S THEREOF


```

Db      1679  AATCATGCCAATGGCCCTCACGTTGGTGCTAGAGCTCACCAGCTAGTGTGAGGGGATAT 1738
Qy      246  AsnTpcCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db      1739  AACTGGTGCCATGACCGGAATGTAGTAACGATTTTCAGTCTCCAACTATTGTTAICGT 1798
Qy      266  CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285
Db      1799  TGTGGTAACCAAGTCGAATCATGGAACTTCAGCACTCTAAATACTCTTTCTTGCAG 1858
Qy      286  PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
Db      1859  TTTGACCCAGCACTCTGAGGCGGACCACTGTACTCGTCGTACCCAGACTACTTC 1918
Qy      306  Leu 306
Db      1919  CTG 1921

RESULT 6
US-09-949-016-5464
; Sequence 5464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERE
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5464
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5464

```

Qy		106	AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrG	:::::
Db		332	GAAcGCATTA CAATTATTGAGAGGAATCACGAAACCCACAATAACCA	
Qy		126	PheTrpAspGluCysLeuArgLysTrgLVsnAlaAsnValTrpLysTr	
Db		392	TTTTTATGATGANTGTCTGCCAAGATATGGGAATGCCAACGTTTGGAATA	
Qy		146	LeuPheAspTrpLeuProLeuThrAlalaLeulleGluHISGluIlePheCy	
Db		452	CTCTTTGATTCTTCACCTTTACAGCTTTTAGTAGATGCACAGATATTCTG	:::::
Qy		166	GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspAr	
Db		512	GGCCTCTCTCCATCCATAGACACACTGGGATCATATAAGAGCGCTCGGATCC	
Qy		186	ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAs	
Db		572	GTTCACATGAGGGGCCCAATGTGTGATCTGTTATGCTCAGATCCAGATGA	
Qy		206	TrpGlyIleSerProArgGlyAlaGlyTrpThrPheGlyGlnAspileAl	
Db		632	TGGGGTATTTACCACCGCTGGTGTGGCTACACATTTGGACAAGACATTTC	
Qy		226	AsnHisThrAsnGlyLeuSerLeuValalaaArgAlaHisGlnLeuValMe	
Db		692	AACATGCCAATGGTGCTCACACTGGTTTCTCGTGCCCCACAGCTTGTAAI	
Qy		246	AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTy	
Db		752	AAITGGTGT CATGATCGGAATGTGGTTACCATTTCAGTGCACCCCNAITPA	
Qy		266	CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe	
Db		812	TGTGGGAAC CAGGCTGCTATCATGGAAATTAGATCACCTTTAAAAATATTTC	
Qy		286	PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr	
Db		872	TTTGACCCAGCGCCTCGTGTGGTGGAGCCTCATGTTACACGGCGCACCCC	
Qy		306	Leu 306	
Db		932	CTA 934	

```

RESULT 7
US-09-949-016-590
; Sequence 590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 590
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-590

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IS THEREOF.

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Percent Similarity: 93.69% Conservatives: 34
Best Local Similarity: 82.39% Mismatches: 19
Query Match: 84.49% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-949-016-590 (1-1541)

QY 6 AspValAspArgGlnIleGlnLeuSerGluCysLysProLeuSerGluLeuGluVal 25
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 46 GAGTGGACCAAGTGGTGGACAGCTGAACAGAGTGAAGCAGCTGAACGAAACAAGTG 105
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTyrAsnValGlnProVal 45
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 106 CGGACGCTGTCGGAGAGCAAGAAATTTTACAAAAGAAATCAATGTGCAAGAGTT 165
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 166 CGTTGCCCTGTTACTGTCGTGGAGATGTCATGCTCAATTTTCATGATCTTTATGGAATC 225
QY 66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 226 TTTAGAATTTGGTGAATAATCAACCGATACAACTACTTTATTCATGGGTGACTATGTAGAC 285
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg 105
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 286 AGAGATATATTCAGTGGAGACTGTGACTCTTCTGTAGCATTAAGAGTGGCTTATCCA 345
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIleThrGlnValTyrGly 125
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 346 GAACGATTAACAATATTCAGAGGAATCACGAAAGCCGACAAATTTACCCAAATATATGGC 405
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyrLysTyrPheThrAsp 145
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 406 TTTTATGATGAATGTCTCGAAGATATGGGAATGCAACAGTTTGGAAATATTTACAGAT 465
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 466 CTCCTTGATATCTTCCACTTACAGCTTTAGTAGATGACAGATATCTGCTCTCATGGT 525
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu 185
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 526 GGCCTCTCTCCATCCATAGACACACTGGATCATATAAGAGCCCTGGATCGTTTACAGGA 585
QY 186 ValProHisGlyGlyProMetCysAspLeuLeuTyrSerAspProAspAspArgCysGly 205
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 586 GTTCCACATGAGGGCCCAATGTGATCTGTATGGTCAGATCCAGATGATCGTGGTGA 645
QY 206 TrpGlyIleSerProArgGlyValaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe 225
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 646 TGGGTATTTTCCACACGCTGGTGGCTACACATTTTGGACAAAGACATTTCTGAAACCTTT 705
QY 226 AsnHisThrAsnGlyLeuSerLeuValaArgAlaHisGlnLeuValMetGluGlyTyr 245
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 706 AACCATGCCAATGGTCTCACACTGGTTCTCGTGCCACCAGCTTGTAAATGGAGGGATAC 765
QY 246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 766 AATTGGTGTCTGATPCGGAATGTGTTTACCATTTTCAGTGCACCAATTTACTGTTATCGT 825
QY 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 826 TGTGGGAACCAAGCTGCTATCATGGAATAGTAGACACTTTTAAATATATCTCTCTTCAA 885
QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 886 TTTGACCGGGCCCTCGTCTGTTGAGCTCATGTTTACACGGCGCACCCAGACTACTTC 945
QY 306 Leu 306
DQ 946 CTA 948

RESULT 8
US-09-780-049-10
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```
; Sequence 10, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHAT
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 10
; LENGTH: 1781
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196) ... (1125)
US-09-780-049-10

Alignment Scores:
Pred. No.: 4.98e-170 Length: 1781
Score: 1411.00 Matches: 250
Percent Similarity: 93.69% Conservatives: 32
Best Local Similarity: 83.06% Mismatches: 19
Query Match: 84.49% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-780-049-10 (1-1781)

QY 6 AspValAspArgGlnIleGlnLeuSerGluCysLysProLeuSerGln 1 25
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 220 GAGTGGACCAAGTGGTGGACAGCTGAACAGAGTGAAGCAGCTCTCCGA 17 279
QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTyrAsnVal 1 45
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 280 AAGAGCCCTCGAGAGAGGCTAAAGAAATCTGACAAAAGAAATCCACAGT 17 339
QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeu 1 65
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 340 CGATGTCAGTCACTGTGTGTGGAGATGTACATGGCAATTTTCATGATCT 17 399
QY 66 PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAsp 1 85
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 400 TTTAGAATTTGGTGTAAATCAACAGATACAAATTTACCTGTTTATGGAGA 17 459
QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysVal 1 105
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 460 AGAGATATTTACTCTGTTGAAACAGTTACACTGCTTGTAGCTCTTAAGGT 17 519
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIleThrGln 1 125
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 520 GAGCGCATCACCATCACTCTCGAGGGAATCACGAGAGCAGACAGATCACACA 17 579
QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyrLysTyr 1 145
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 580 TTCACGACGAGTGTTTAAGGAATACGGAATGCAAAATGTTTGGAAATA 17 639
QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGlyIlePheCys 1 165
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 640 CTTTTTGACTATCTTCTCTCCTCTCAGTGGCTTGGTGGAGAGATCTTCTG 17 699
QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArg 1 185
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 700 GGTCTGTCCATCCATAGACACACTGGATCACATCCGAGCAGCTCGATCG 17 759
QY 186 ValProHisGlyGlyProMetCysAspLeuLeuTyrSerAspProAspAsp 1 205
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 760 GTTCTCATGAGGGTCCAAATGTGTGACTTGTGTGTCAGATCCAGATGAA 17 819
QY 206 TrpGlyIleSerProArgGlyValaGlyTyrThrPheGlyGlnAspIleAla 1 225
DQ ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
DQ 820 TGGGGGATATCTCTCTCGGGAGCTGGTTATACCTTTTGGCCAAGATATTTTC 17 879
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```
QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
|||
DB 880 AATCATGCCAATGGCTCAGCTGGTGTCCAGAGCTCACCAGCTGGTATGAGGAGAT 939

QY 246 AsnTrpCysGlnAspGlyAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
|||
DB 940 AACTGGTGCATGACCGGAACGTAGTAAACAATTTTCAGTGTCTCCAAACTATTGCTATCGT 999

QY 266 CysGlyAsnMetAlaAlaMetGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 285
|||
DB 1000 TGTGTAACCAAGCTGCAATCATGGAACCTTGACGACACTCTTAAAGTATTCTTTCTTGCGAG 1059

QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
|||
DB 1060 TTTGACCCAGCACCTCGTAGCGCGACCATGTCATCGTGTGTAACCCAGACTACTTC 1119

QY 306 Leu 306
|||
DB 1120 CTG 1122

RESULT 9
US-09-780-045-10
; Sequence 10, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT B
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0130
; CURRENT APPLICATION NUMBER: US/09/780,045
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 10
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (310)...(1239)
US-09-780-045-10

Alignment Scores:
Pred. No.: 5,26e-170 Length: 1843
Score: 1411.00 Matches: 248
Percent Similarity: 93.69% Conservative: 34
Best Local Similarity: 82.39% Mismatches: 19
Query Match: 84.49% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-780-045-10 (1-1843)

QY 6 AspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeuGluVal 25
|||
DB 334 GAGCTGGACCACTGGGTGGAGAGCTGAACAGTGTAAAGCAGCTGAACGAGAACCAAGTG 393

QY 26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProVal 45
|||
DB 394 CGGACGCTGTGCGAAGCGTAAAGAAATTTTAAACAAAGAAATCAATGTACAAAGAGTT 453

QY 46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu 65
|||
DB 454 CGCTGTCTCTTACCTGTGTGGAGATGTGATGGCCAAATTCATGACCTTATGGAATC 513

QY 66 PheArgIleGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
|||
DB 514 TTCAGAAATGGTGGAAATCAACAGACCACTATCTATTCTATGCTGGTGTATGATGAC 573

QY 86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg 105
|||
DB 574 AGAGGATATTAATCTGTGGAGACCGTGTACTCTTCTGTAGCAATTAAGAGTGTGCTATCCA 633
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```
QY 106 AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlu 125
|||
DB 634 GAGCTATACANATATTCGAGGAAATCATGAAAGCCGCGCAGATCACACA 693

QY 126 PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyr 145
|||
DB 694 TTTTATGATGAATGCTACGAAAGTATGGAACGCGCAACGCTGTGGAATA 753

QY 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCys 165
|||
DB 754 CTCCTTGATTAATCTTCCACTTACAGCTTTAGTAGATGACAGATATTTCTG 813

QY 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArg 185
|||
DB 814 GGCCTCTCTCCATCCATAGATACACTGGATCACATAAGAGCCCTCGATCG 873

QY 186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAs 205
|||
DB 874 GTTCACATGAGGCGCCAAATGTGTATCTTATGTGTGATGCCAGATGA 933

QY 206 TrpGlyIleSerProArgGlyValAlaGlyTyrThrPheGlyGlnAspIleAl 225
|||
DB 934 TGGGCAATTTCTCCACGTGGTGTGCTGCTACACATTTGGACAGACATTTTC 993

QY 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMe 245
|||
DB 994 AACCATGCCAACGGCTCACACTGGTGTCCGCTGCTACACAGCTGTGTAAT 1053

QY 246 AsnTrpCysGlnAspLysAsnValValThrPheSerAlaProAsnTyr 265
|||
DB 1054 AATTTGGTGCATGATCGGAATGTGTCCACCATTTTGTAGTGACCCCAATTA 1113

QY 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSe 285
|||
DB 1114 TGTGGAAACAGGCTGTCTATCATGGAATTAGACGACACTTTAAATACTC 1173

QY 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 305
|||
DB 1174 TTTGACCCAGCACCTCGTGTGGAGAGCTCATGTGACCCCGCGCACCCC 1233

QY 306 Leu 306
|||
DB 1234 CTA 1236

RESULT 10
US-09-780-045-3
; Sequence 3, Application US/09780045
; Patent No. 6602713
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATA
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0130
; CURRENT APPLICATION NUMBER: US/09/780,045
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 3
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (991)...(1920)
US-09-780-045-3

Alignment Scores:
Pred. No.: 8,96e-170 Length: 2574
Score: 1411.00 Matches: 248
Percent Similarity: 93.69% Conservative: 34
Best Local Similarity: 82.39% Mismatches: 19
Query Match: 84.49% Indels: 0
DB: 3 Gaps: 0
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US-10-764-259-13 (1-306) x US-09-780-045-3 (1-2574)

Qy	6	AspValAspArgGlnIleGluInLeuSerGluCysLysProLeuSerGluLeuGluVal	25
Db	1015	GAGCTGGACCAGTGGGTTCGAGCAGCTGAACGAGTGTAAAGCAGCTGAACGAGAACCAAGTG	1074
Qy	26	LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProVal	45
Db	1075	CGGACGCTGTGCGAGAAAGGCAAAAGAAATTTTAAACAAAGAAATCAAAATGTGCAAGAGGTT	1134
Qy	46	LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuIleGluLeu	65
Db	1135	CGTTCGCTCTTACTGTCTGTGGAGATGTGCATGGTCAATTTTCATGATCTTATGGAACTC	1194
Qy	66	PheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp	85
Db	1195	TTTAGAAATGGTGGAAATCACCGGATACAAACTACTTATTCATGGGTGACTATGTAGAC	1254
Qy	86	ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg	105
Db	1255	AGAGGATATTATTTCAGTGGAGACTGTGACTCTTCTGTAGCATTTAAAGGTGCGTTATCCA	1314
Qy	106	AspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGly	125
Db	1315	GAACGCATTTACAATATTGAGAGGAATTCAGAAAGCCGACAAATTCACCAAGTATATGGC	1374
Qy	126	PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAsp	145
Db	1375	TTTTATCATGAATGTCGCGAAAGTAGTGGAAATGCCAACCTTTGGAAATATTTACAGAT	1434
Qy	146	LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly	165
Db	1435	CTCTTTGATTATCTTCCACTTTACAGCTTTTAGTAGACACAGATATTTCTGCCTCCATGGT	1494
Qy	166	GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu	185
Db	1495	GGCCTCTCTCCATCCATAGACACACTGGATCATATAAGAGCCCTGGATCGTTTACAGAA	1554
Qy	186	ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly	205
Db	1555	GTCCACATGAGGGCCCAATGCTGTGATCTGTATGGTCAGATCCAGATGATCGTGGTGA	1614
Qy	206	TrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluInPhe	225
Db	1615	TGGGGTATTTCCACACGTGTGTGGGTGCACATTTGGACAAGACATTTCTCTGAACCTTT	1674
Qy	226	AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr	245
Db	1675	AACCATGCCAATGGTCTCACACTGGTTTCTCGTCCCAACCACTGTGAATGGAGGGATAC	1734
Qy	246	AsnTrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg	265
Db	1735	AATTTGGTGTATGATGCGAATGTGTTTACCAATTTTTCAGTCACCAATTTACTGTTATCGT	1794
Qy	266	CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln	285
Db	1795	TGTGGGAACCAAGGCTGCTATCATCGAATTTAGATGACACTTTTAAAAATATTCCTCTTCAA	1854
Qy	286	PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe	305
Db	1855	TTTGACCCAGCGCTCGTGGTGGACCTCATGTTACGGCGACCCACAGACTACTTTC	1914
Qy	306	Leu 306	
Db	1915	CTA 1917	

RESULT 11

US-09-190-976B-11
; Sequence 11, Application US/09190976B
; Patent No. 6815187
; GENERAL INFORMATION:
; APPLICANT: Simons, Michael

```

; Horowitz, Arie
TITLE OF INVENTION: Stimulation of angiogenesis via
; syndecan-4 cytoplasmic domain signa
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/190,976B
FILING DATE: 12-No. 6815187-1998
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-190-976B-11

Alignment Scores:
Pred. No.:      2,71e-164      Length:      1721
Score:          1366.00        Matches:     247
Percent Similarity: 92.36%    Conservative: 31
Best Local Similarity: 82.06% Mismatches:   23
Query Match:     81.80%      Indels:      1
DB:              3           Gaps:        0

US-10-764-259-13 (1-306) x US-09-190-976B-11 (1-1721)

Qy      6 AspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGlu
Db      128 GAGCTGGACCGTGGATCGGACGAGTGCAACAGTCGAACGACTGTCTGTA
Qy      26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnVa
Db      188 AAGAGCCCTCTGCAGAAGGCTAAAGAAATCCTGGACAAAAGAAATCCAATGT
Qy      46 LysCysProValThrValCysGlyVasPleHisGlyGlnPheHisAspLei
Db      248 CGATGCCAGTCACTGTTCGTGGAGATGTGCATGGGCAATTTTCATGATCT
Qy      66 PheArgIleGlyLyAsAlaProAspThrAsnTyrLeuPheMetGlyVas
Db      308 TTTAGAATTGGTGGCAATACCAGATACAAATTACTTGTATTATGGGCGCA
Qy      86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValalaLeuLysVa
Db      368 AGAGGATATTATTTCAGTGGAAACAGTTACTTCTGCTTAGCTCTTAAGGT
Qy      106 AspArgIleThrIleLeuArgGlyVasHisGlySerArgGlnIleThrGlu
Db      428 GAACGTATCACCATTTCTTCAGGAAATCATGAGACGACAGATCACACA
Qy      126 PheTyrAspGluCysLeuArgLysTyrGlyVasAlaAsnValTrpLysTy
Db      488 TTCTACATCAGTGTCTTAAGAAATAACGAAATGCAAATGTTTGGAAAGTA

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Qy 146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165
Db CTTTITGACTATCTCTCTCACTGCTTGGTGATGGCGAGCATCTTCTGTACATGGT 607
Qy 166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlu 185
Db GGCCTCTCACCATCCATAGATACACTGGATCAGATCAGAGCAGCTTGTATCGCCACAGAA 667
Qy 186 ValProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAspArgCysGly 205
Db GTTCTCTATGAGGTCCATGTGACCTTCTGTGCTGATCCAGATCCAGATCCAGATCCAGAT 727
Qy 206 TrpGlyIleSerProArgGlyValaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe 225
Db TGGGGTATATCTCTCGAGGAGCTGTTACACCTTTTGGCGAGGATATTTCTGAGACATTT 787
Qy 226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
Db AATCATGCAATGGCTCAGCTTGGTGTCTAGAGCTCATCAGCTGCTGATGGAGGATAT 847
Qy 246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db AACTGTGCCATGACCGAAATGTAGTAAAGATTTTACGTGCTCCAAACTATTTGTTATCGT 907
Qy 266 CysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPheLeuGln 285
Db TGTGTACCAAGCTGCAATCATGGAATCTGATGATCTCTAAATACTCTTTCTTGCAG 967
Qy 286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPhe 305
Db TTTGACCCAGCAGCCGC-AGAGGCGAGCCACATGTTACTCGTGTACCCAGACTACTTTC 1026
Qy 306 Leu 306
Db 1027 CTG 1029

RESULT 12

US-09-487-558B-269
; Sequence 269, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 269
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-269
Alignment Scores: 5.53e-155 Length: 1134
Pred. No.: 1291.00 Matches: 229
Score: 87.67%
Percent Similarity: 87.67%
Conservative: 34

Best Local Similarity: 76.33% Mismatches: 37
Query Match: 77.31% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-487-558B-269 (1-1134)

Qy 7 ValAspArgGlnIleGluGlnLeuSerGluCysLysProLeuSerGluLeu 26
Db CTTGACCAATGGATTGAGCATTTGAGTAAATGCGAGCCACATATCAGAAGA 291
Qy 27 AsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTyrAsnValIcI 46
Db CGACTATGATAAAATGGCGGTGGACGTGTTCAGTTCGAGGAGAAATGTTAA 351
Qy 47 CysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuI 66
Db GTGCTGTTCACATTTGTGGTGACGTACACGGTCNAATTCATGACTTGT 411
Qy 67 ArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMetGlyAspTy 86
Db AAGATTGGTGGTCTTGTCTGACACCAATTTACCTTTTCATGGGTGATT 471
Qy 87 GlyTyrTyrSerValGluThrValSerLeuValAlaLeuLysValAr 106
Db GGATATTATCTGTGAGACCGTATCTTACCTAGTTGCCATGAAAGTCAG 531
Qy 107 ArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIleThrGlnVa 126
Db AGAATTACTATCTTAGGGCAATCACGAGTCTAGGCAGATTACCCAAGT 591
Qy 127 TyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTyrLysTyrPh 146
Db TATGACCAATGTTTGAGAAAGTACGGCAGTCGCAACGTTGGAAATGTT 651
Qy 147 PheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLe 166
Db TTCGATTATTTCCCGGTTACTGCGCTTGGTGGATAATAAAATCTTCTGTT 711
Qy 167 LeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgI 186
Db CTCTCACCCTATGATAGACAACTAGATCAAGTTAGAGATTTAAATAGAA 771
Qy 187 ProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAspAr 206
Db CCTCAGCAAGGTCCCAATGTTGTGACCTTCTATGGTCCGATCTCTGATGAT 831
Qy 207 GlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaG 226
Db GGAATCAGTCCGAGAGGTGCGAGGCTTCACTTTTGGTCAAGACATCAGTGA 891
Qy 227 HisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetG 246
Db CACACTAATGACCTATCACTAATAGCAAGACTCACCNAATTTGGTAAATGGA 951
Qy 247 TrpCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCy 266
Db TGGTCTCACCAGCAAAATGTTGTCCACCTTTTCAGTGTCTCCAAATATTG 1011
Qy 267 GlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsnArgSerPh 286
Db GGTAACCCAGGCGCTATTATGAGGTGGATGAAACCAATAATAGGCAAT 1071
Qy 287 GluProAlaProArgGlnSerGluProAspValThrArgLysThrProAs 306
Db GATCCATCTGTGAGACCGGCTGAAACCAACCGTCCACGAGAAAGACCCGGA 1131

RESULT 13

US-09-614-221A-47
; Sequence 47, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk


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QY 107 ArgileThrIleuArgGlyAenHisGluSerArgGlnIleThrGlnValTyrGlyPhe 126
DB 508 AGAATTCAGTACTAGAGCCATACAGAGTCTAGGCAGATACCAAGTATACGGGTTT 567
QY 127 TyrAspGluCysLeuArgGlyTyrGlyAenAlaAenValTyrPheThrAspLeu 146
DB 568 TATGATGAATGTTTGAGAAAGTACGGCAGTGCACAACTGTGGAATAATGTTACAGATCTT 627
QY 147 PheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGly 166
DB 628 TTCGATTATTTCCATATACCGCATAGTAGATAATAAATTTCTGCTGCATGAGGA 687
QY 167 LeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluVal 186
DB 688 CTTTCCCCCATGATAGAACCATAGATCAGGTGAGAGATTGACAGAAATACAGGAGTG 747
QY 187 ProHisGluGlyProMetCysAspLeuLeuTyrSerAspProAspAspArgCysGlyTyr 206
DB 748 CCTCATGAAGTCTTATGTGTGACCTTCTATGTCAGACCTTGACGATAGAGCGGATGG 807
QY 207 GlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAen 226
DB 808 GGAATCAGTCCCAGAGGTGCAGCTTCTATGTCAGACCTTGACGATAGAGCGGATGG 867
QY 227 HisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsn 246
DB 868 CACACTAATGATCTATCACTAATAGCAGAGCTCACCATTGTTGTAAGGCTATGCT 927
QY 247 TrpCysGlnAspLeuValThrValPheSerAlaProAsnTyrCysTyrArgCys 266
DB 928 TGGTCTCACCAGCAAAATGTTGTCACCACTTTTTCAGTGTCTCTTAATTTACTGCTACAGATGT 987
QY 267 GlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGlnPhe 286
DB 988 GGTAAATCAAGCAGCTATCATGAAAGTGGACGAGAAATCAATATAGACAAATTTCTTACAGTAC 1047
QY 287 GluProAlaProArgGlnSerGluProAspValThrArgLysThrProAspTyrPheLeu 306
DB 1048 GACCCATCCGTAAAGCAGGTGAACTAGCTGACAGAAAGACCCAGATTACTTTTATA 1107

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RESULT 15

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US-09-949-016-2909
; Sequence 2909, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2909
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2909

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Alignment Scores:

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Pred. No.: 3,19e-135 Length: 1339
Score: 1137.50 Matches: 204
Percent Similarity: 81.43% Conservative: 46
Best Local Similarity: 66.45% Mismatches: 56
Query Match: 68.11% Indels: 1
DB: 3 Gaps: 1

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US-10-764-259-13 (1-306) x US-09-949-016-2909 (1-1339)
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys eu 20
DB 104 ATGGCGGAGATCAGCGAGCTCGACGGCAGATCGAGCAGCTGCGTCGCTG TC 163
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal tp 40
DB 164 AAGGAGAGCGAAGTCAAGGCCCTGTGCGCTAAGGCCAGAGAGATCTTGGT GC 223
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly is 60
DB 224 AACGTGCAGAGGGTGGACTCGCCAGTCACAGTGTGCGCGCAGCATCCATGG AT 283
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr et 80
DB 284 GACCTCAAGAGCTGTTTCAGAGTAGGTGGCGACGTCCCTGAGACCAACTA TG 343
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe eu 100
DB 344 GGGGACTTTGTGGACCGTGGCTTCTATAGCGTCGAAACGTTCCCTCCTGCT TT 403
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe le 120
DB 404 AAGGTTCTGCTATCTGATCGCATCACACTGATCGGGGCAACCATGAGAG TC 463
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl tp 140
DB 464 ACGGAGGTCTATGGCTTCTACGATGAGTGTCTGCGCAAGTACGGCTCGGT GG 523
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGly le 160
DB 524 CGCTACTGCATCGAGATCTTTGACTACTCTAGCCTGTGAGCCATCATCGA TC 583
QY 161 PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIle le 180
DB 584 TTCTCGGTGACCGGGGCTCTCCCTCCATCCAGACCTCGGATCAGAT TC 643
QY 181 AspArgIleGlnValProHisGluGlyProMetCysAspLeuLeuTyr ro 200
DB 644 GACCGAAAGCAAGAGGTGCTCATGATGGGCCCATGTGTGACCTCCTCTG CA 703
QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh sp 220
DB 704 GAAGACACACAGGCTGGGGGTGAGCCCCCGAGGAGCGGCTACCTATT AC 763
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl eu 240
DB 764 GTGGTGGGCCAGTTTCAACGCGACCAATGCATTCACATGATGATGTCGCTGC TG 823
QY 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPh ro 260
DB 824 GTGATGGAAGGTTTCAAGTGGCCTTCAATGAGACGGGTGCTCCTGTGTG CC 883
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGly sn 280
DB 884 AACTACTGCTACCGCTGTGGAAATGTGGCACCCATCTTGGAGAGCTGGACGA AG 943
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa ys 300
DB 944 AAAGATTTCATCATCTTTGAGGCTGCTCCCAAGACACACGGGGCATCCC AG 1003
QY 301 ---ThrProAspTyrPheLeu 306
DB 1004 CCCGTGGCCGACTACTTCTCTG 1024

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Search completed: December 9, 2005, 12:58:23
Job time : 212 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:28:16 ; Search time 825 Seconds
(without alignments)

3067.187 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670

Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPRQSPDVTRKTPDYFL 306

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=PublishedApplications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm

-MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRESH=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.Main:

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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*

8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1670	100.0	1365	7	US-10-764-259-8
3	1549	92.8	1386	6	US-10-236-699-21
4	1547	92.6	1330	6	US-10-236-699-31
5	1521	91.1	1243	6	US-10-236-699-7
6	1521	91.1	1525	8	US-10-425-115-160542
7	1518	90.9	1732	7	US-10-425-114-35277

8	1508.5	90.3	1195	7	US-10-437-963-40723	Sequ
9	1508.5	90.3	1298	6	US-10-236-699-25	Sequ
10	1508	90.3	921	3	US-09-938-842A-705	Sequ
11	1508	90.3	921	3	US-09-938-842A-705	Sequ
12	1495	89.5	924	3	US-09-938-842A-571	Sequ
13	1495	89.5	924	3	US-09-938-842A-571	Sequ
14	1478	88.5	1879	8	US-10-425-115-149113	Sequ
15	1456	87.2	1759	8	US-10-425-115-160546	Sequ
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17	1452	86.9	1759	7	US-10-424-599-20866	Sequ
18	1431	85.7	1626	7	US-10-425-114-28862	Sequ
19	1431	85.7	1734	8	US-10-425-114-28862	Sequ
20	1429	85.6	1484	8	US-10-425-115-149110	Sequ
21	1427	85.4	1738	6	US-10-739-930-1189	Sequ
22	1427	85.4	1738	6	US-10-388-934-574	Sequ
23	1427	85.4	1804	3	US-10-291-808-39	Sequ
24	1427	85.4	1804	3	US-09-917-800A-1624	Sequ
25	1427	85.4	1804	7	US-10-191-803-83	Sequ
26	1427	85.4	1804	9	US-10-386-971-2	Sequ
27	1427	85.4	2181	6	US-10-007-926A-184	Sequ
28	1427	85.4	2181	7	US-10-467-126-17	Sequ
29	1427	85.4	2181	9	US-10-936-273-20	Sequ
30	1411	84.5	2966	7	US-10-467-126-3	Sequ
31	1411	84.5	1531	6	US-10-210-120-42	Sequ
32	1411	84.5	1531	9	US-10-909-035-42	Sequ
33	1411	84.5	1541	9	US-10-956-157-1198	Sequ
34	1411	84.5	1580	6	US-10-388-934-575	Sequ
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39	1411	84.5	2574	7	US-10-467-008-10	Sequ
40	1408	84.3	1487	6	US-10-467-008-3	Sequ
41	1408	84.3	1529	3	US-10-236-699-23	Sequ
42	1404	84.1	1279	6	US-09-880-107-2098	Sequ
43	1392	83.4	1263	7	US-10-236-699-2	Sequ
44	1392	83.4	2720	8	US-10-311-764-14	Sequ
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ALIGNMENTS

RESULT 1

US-09-828-302-8
; Sequence 8, Application US/09828302
; Patent No. US20020152502A1
; GENERAL INFORMATION:
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND N
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-302-8

Alignment Scores:
Pred. No.: 3.52e-216 Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-764-259-13 (1-306) x US-09-828-302-8 (1-1365)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGlyCysLysProLeu 20
DB ATGCCGTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTCGAGTGCAGCCGTTG 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
DB TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGACCATCTTGGTGGAGAGTGG 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB AACGTGACGCCGTCGAAGTGTCTGTACGGTTTCGGGTGACATCCATGGCCAGTTTCAT 250
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
DB GATCTCATCGAGCTTTCCGCATAGAGGCAAGGCCCGCCGACACGAACTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
DB GCGCAGCATATGTGATCGTGATATATTCTGTGAGAGACTGTGTGCTCTTAGTGGCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB AAGGTGCGGTATAGGATAGGATCAACATCTTCGAGGGGAACCCAGAGCAGGCAGATT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB AGCAAGTATATGTTTCTATGATGAATGCTCTCGGAGTAGTGGAAATGCCAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrIleProLeuThrAlaLeuIleGluHisGluIle 160
DB AAGTACTTTCACGATCTGTGACTACCTGCTCTGACAGCTCTCATTTGACGACGAGATT 550
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB TTTTGTCTTCATGGTGGTGTGCTCCATCGCTCGACACATTAGATCATCCGAGCCCTA 610
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuTrpSerAspPro 200
DB GATCGTATTCAGAAAGTCCGCGCACGAGGGCCGATGTGTGATCTACTCTGGTCTGATCCA 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB CATGATCGTTGTGGATGGGGCATTTCCACCAGAGTGGCGGTTATACITTTGGTCAAGAT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB ATTGCAGAGCAGTTCATCATACCAATGGTCTAAGTTTGGTTGACGCTGCTCACCAGCTT 790
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
DB GTGATGGGAAGGATACAATTTGGTGGCAGGATAAAATGTTGTCCACAGTTTTCAGTGCCTCC 850
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGluThrMetAsn 280
DB AATTAATCTGTATACCGTGTGGGAACATGGCCGCATAAATGGAGATAGATGAACATGAAT 910
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
DB CGGTCTTTTCTTCAGTTGCAACAGACCGCCGCGCAAGTGAACACAGATGTGACCGCGAAG 970
QY 301 ThrProAspTyrPheLeu 306
DB ACTCCTGATTACTTTCG 988
```

RESULT 2

US-10-764-259-8
; Sequence 8, Application US/10764259
; Publication No. US20040148658A1
; GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA

```
; APPLICANT: VAN THIELEN, NOCHA  
; APPLICANT: CHEN, ROUYING  
; APPLICANT: ISHITANI, MANABU  
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND M  
; TITLE OF INVENTION: IN PLANTS  
; FILE REFERENCE: 16313-0029  
; CURRENT APPLICATION NUMBER: US/10/764, 259  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: 60/196,001  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 1365  
; TYPE: DNA  
; ORGANISM: Physcomitrella patens  
US-10-764-259-8
```

Alignment Scores:
Pred. No.: 3.52e-216 Length: 1365
Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-764-259-13 (1-306) x US-10-764-259-8 (1-1365)

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QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys 20
DB 71 ATGCCGTCATATGCAGATGTAGACCGGCAGATAGACAGCTGTCGAGTGT 130
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
DB 131 TCGGAGTTGGAGGTGAAGAACCTATGTGATCAAGCTCGACGATCTTGGT 190
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60
DB 191 AACGTGACGCCGTCGAAGTGTCTCGCTGACGGTTTGGGTGACATCCATGG 250
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr 80
DB 251 GATCTCATCGAGCTTTCCGCATAGAGGCAAGGCCCGCCGACACGAACTA 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 311 GCGGACTATGTGGATCGTGGATATATTCTGTCGAGACTGTGTGCTCTT 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe 120
DB 371 AAGGTGCGGTATAGGATAGGATCACAACTCTTCGAGGGGAACCCAGAGAG 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAla 140
DB 431 ACGCAGTATATGTTTCTATGATGAATGCTCTCGGAGATATGGAATGCT 490
QY 141 LysTyrPheThrAspLeuPheAspTyrIleProLeuThrAlaLeuIleGly 160
DB 491 AAGTACTTTCACGATCTGTTTCGACTACCTGCTCTGACAGCTCTCATTTG 550
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 180
DB 551 TTTTGTCTTCATGGTGGTGTCTCTCCATCGCTCGACACATTAGATCATCC 610
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuTrp 200
DB 611 GATCGTATTCAGAAAGTCCGCGCACGAGGGCCGATGTGTGATCTACTCT 670
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPhe 220
DB 671 GATGATCGTTGTGGATGGGGCATTTTCACCAGAGTGGCCGTTATACITTT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAla 240
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Db 731 ATTGCAGACAGTTCATCATACCAATGCTCTAAGTTTGTCAGCGTCTCACCAGCTT 790
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 791 GTGATGAAGGATACAAATGGTGCCAGGATAAAATGTTGTCCACAGTTTTTCAGTGCCGCC 850
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaMetGluLeuAspGluThrMetAsn 280
Db 851 AATTACTGTTACCGTGTGGGAACATGGCCGCATTAATGGAGATAGATGAACAATGAT 910
Qy 281 ArgSerPheLeuGlnPheGluProAlaProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 911 CGGTCTCTTTCTTCAGTTCGAACAGCAGCCGCGCAAGTGAACCCAGATGTGACGCGGAG 970
Qy 301 ThrProAspTyrPheLeu 306
Db 971 ACTCCTGATTACTTTCTG 988

RESULT 3
US-10-236-699-21
; Sequence 21, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Glycine max
US-10-236-699-21

Alignment Scores:
Pred. No.: 1,11e-199 Length: 1386
Score: 1549.00 Matches: 280
Percent Similarity: 96.73% Conservative: 16
Best Local Similarity: 91.50% Mismatches: 10
Query Match: 92.75% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-236-699-21 (1-1386)
Qy 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
Db 92 ATGCGCTCTCAGCGGATCTGGAGGACAGATCGAGCGCTGATGGACTGCAAGCTCTG 151
Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
Db 152 TCGGAGTCGGAGTGAAGCGCTGTGCGATCAAGCGGAGGACGATTTCTTGTGGAGGAGTG 211
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
Db 212 AACGTGCAACCGGTTAAGTCCCGTCCCGTCCCGGATATTCACGCCAGTCTAC 271
Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
Db 272 GATCTCATCGAGCTGTTTCGGATTGGAGGACGCTCCCGATACCAATATCTCTTCATG 331
Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
Db 332 GGTGATTATGATAGTCGTGGATCTATTTCAGTGGAGACTGTTACACTTTTGGTGCGCTTTG 391
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Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSer 120
Db 392 AAGTCCCTTTATAGAGATAGAAATCAATTTCTCAGGGGAAATCATGAAAG 451
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl 140
Db 452 ACTCAAGTGTATGGCTTCTATGATGAATGCTTGAGAAAATATGGAATGC 511
Qy 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleG 160
Db 512 AAATACITTTACAGACTTCTTTGATTTATTTGCTCTGACTGCCCTCATTTGA 571
Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI 180
Db 572 TTTCTGCTTGCATGGAGGTCTCTCACCTTCTTTGGATACACTGGATAACA 631
Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr 200
Db 632 GATCGTATTCAAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTTGTG 691
Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh 220
Db 692 GATGATCGCTGTGGATGGGAATATCTCCACGTGGTGCAGGATACACAT 751
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl 240
Db 752 ATAGCTGCTCAGTTTAAATCATACCAATGGCTCTCTCCCTGATATCGAGAG 811
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh 260
Db 812 GTTATGGAAGGATTCAATTGGTGGCAGGACAAAGAAATGTGGTGACTGTATT 871
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGl 280
Db 872 AATTACTGTTATCGATGTGGGAATATGGCTGCCCATCTAGAAATAGGAGA 931
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa 300
Db 932 CAGAAATTTTTCAGTTTGATCCAGCTCCAGGCCAATTTGAGCCTGACAC 991
Qy 301 ThrProAspTyrPheLeu 306
Db 992 ACTCCAGATTTATTTTG 1009

RESULT 4
US-10-236-699-31
; Sequence 31, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPE
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-236-699-31

Alignment Scores:
Pred. No.: 1,95e-199 Length: 1330
Score: 1547.00 Matches: 280
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Percent Similarity: 96.41% Conservative: 15
Best Local Similarity: 91.50% Mismatches: 11
Query Match: 92.63% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-236-699-31 (1-1330)

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QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysIysProLeu 20
DB 104 ATGCGGTCTCACGCGATCTGGAACGACAGATCGAGCAGCTGATGAGTGCAGGCTCTG 163
QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLutrp 40
DB 164 TCGGAGTCGGAGTGAAGCGCTGTGTATCAAGCGAGGCGGATTTCTCGTGAGGAATGG 223
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 224 AACGTGCAACCGTGAAGTGCCTCCGTCACCGTCTCGGCGATATTCACGGCCAGTTTAC 283
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyIysAlaProAspThrAsnTyrIleuPheMet 80
DB 284 GATCTCATGAGCTGTTTCGGATTGAGGGAACGCAACCGATACCAATATCTCTTCATG 343
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
DB 344 GGTGATTATGATAGATCGGTACTATTTCAGTGGAGACTGTTACACTTTTGTGTGCTTTG 403
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB 404 AAGTCCGTTACAGAGATAGATACAAATCTTCAGGGGAATCATGAAGTGTCAATTT 463
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 464 ACTCAAGTGTATGGCTTCTATGATGAATGCTTGAGAAAATATGGAATGCCAATCTCTGG 523
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGluHisGluIle 160
DB 524 AAATACTTTACAGACTGTGTTGATTATTTACCTCTGACTGCCTCATTTGAGAGTCAGATT 583
QY 161 PheCysLeuHisGlyCysLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 584 TTCTGCTTGCATGGAGTCTCTCACCTTTTGGATACACTGGATAACATCAGACATTG 643
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 644 GATCGTATACAAGAGTTCCATCAATGAAGCAACCAATGTGTGATCTCTTGTGTCTGACCT 703
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB 704 GATGATCGCTGTGGATGGGAATATCTCCACGTGTGCAGGATACACATTTTGGACAGGAT 763
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB 764 ATAGCTGCTCAGTTTAATCATACCAATGCTCTCTCCCTGATATCAGAGCTCATCAGTTT 823
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspIysAsnValThrValPheSerAlaPro 260
DB 824 GTTATGGAAGGATTCAAATGGTGCCAGGACAAAATGTGGTGACTGTATTTAGTGACCA 883
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
DB 884 AATTACTGTATCCGATGTGGGAATATGGCTGTATACTAGAAATAGGAGAAATATGGAT 943
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
DB 944 CAGAATTTCTTCAGTTTGATCCAGGCCCCAGGCAAAATGAGCCTTGACACCAACGCAAG 1003
QY 301 ThrProAspTyrPheLeu 306
DB 1004 ACTCCAGATTAATTTTAA 1021
```

RESULT 5

US-10-236-699-7

```
; Sequence 7, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEP
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236,699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-236-699-7
```

Alignment Scores: 6.11e-196 Length: 1243
Pred. No.: 1521.00 Matches: 272
Score: 1521.00 Conservative: 20
Percent Similarity: 95.42% Mismatches: 14
Best Local Similarity: 88.89% Indels: 0
Query Match: 91.08% Gaps: 0
DB: 6

US-10-764-259-13 (1-306) x US-10-236-699-7 (1-1243)

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QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCysIys 20
DB 150 ATGCGGAGAGCGGAGACATCGATCGTCAGATCGAGCAGCTGATCGAGTGT 209
QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
DB 210 TCCGAGGCGGAGGTCAAGACGCTCTGCGAGCAAGCGAGGCGGATTTCTGGT 269
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGly 60
DB 270 AATGTTACGCGGTAAAGTGTCCGTCACCGTCTGCGGCGACATCCACGG 329
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyIysAlaProAspThrAsnTyr 80
DB 330 GATCTGATTGAGCTTTTAAAGTCGGTGTCTTCGCCCTGACACCAATTA 389
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 390 GCGGATTACGTAGATCGAGGGTATTATTCTGTGGAGACAGTCTCGCTCTT 449
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe 120
DB 450 AAAGTTCCTCAGAGATAGGCTTACCATCTTAAGAGGGAATCAGAAAG 509
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAla 140
DB 510 ACTCAAGTGTATGGATTTTATGATGAGTGTCTTGAGAAAATATGGAATGC 569
QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGlu 160
DB 570 AAACACTTCACTGACCTTTTGTATTATCTCTCTTACAGCTCTCATCGA 629
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle 180
DB 630 TTCTGTTTACATGAGGGCTCTCACCTTCTTTAGATACACTTGCACCAAT 689
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrp 200
DB 690 GATCGAATCCAAAGAGGTTCCACATGAAGGACCTATGTGTGATCTCTTTATG 749
```

QY 201 AspAspArgCysGlyTyrPheGlnSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
 DB 750 GATGATCGATCGGTTGGGATAATCTCTCGTGGCGAGGCTACACGTTCCGACAAGAT 809
 QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
 DB 810 ATCGCTACTCAGTTTAACACACACCAATGGACCTCAGTCTGATCTCAAGAGCACACCAACTT 869
 QY 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPheSerAlaPro 260
 DB 870 GTCTGGAAGGTTATTAATTTGGTCCCAAGAAAGACGTTGTGACTGTGTGTAGCGCCCA 929
 QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
 DB 930 AACTATTGCTACCGATGCGGCAACATGGCTGCTATTCTAGAGATAGACGAGAACAATGGAC 989
 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
 DB 990 CAGAAGCTTCCTTCAGTTCCGATCCAGCCCAACGTCAGTAGAAGTAGAACCCGAAACTACGCAAA 1049
 QY 301 ThrProAspTyrPheLeu 306
 DB 1050 ACTCCAGATTACTTTTGG 1067

RESULT 6

US-10-425-115-160542
 ; Sequence 160542, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222) B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 160542
 ; LENGTH: 1525
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(1525)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MPT4577_77994C.1
 US-10-425-115-160542

Alignment Scores:

Pred. No.: 8,43e-196 Length: 1525
 Score: 1521.00 Matches: 272
 Percent Similarity: 96.41% Conservative: 23
 Best Local Similarity: 88.88% Mismatches: 11
 Query Match: 91.08% Indels: 0
 DB: Gaps: 0

US-10-764-259-13 (1-306) x US-10-425-115-160542 (1-1525)

QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysProLeu 20
 DB 246 ATGCATCGACCGGATCTGACCGCCAGATCTGCAGCTCGGGATGCAAGTCTCTG 305
 QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTyr 40
 DB 306 CCTGAGCGGAGGTCAAAACGCTATCGAGCAGCCAGCGCATCTCTCATGGAGGATGG 365
 QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
 DB 366 AACGTGCACCGCGTGGTGGCCCGTCACTGTCTCGGCGCATCCAGCGCCAGTCTTAC 425

QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr
 DB 426 GACCTCATCGAGCTCTTTTCGATCGGTGGCGAGCGCCGACACCAACTA
 QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu
 DB 486 GCGCACTACGTGCGACCGGTGGCTATTACTCACTGGAGACTGTGTCTTAT
 QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSer
 DB 546 AAGTACCTTATAGACAGAGAAATCACATATTTGAGAGGAATCATGAGAG
 QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl
 DB 606 ACTCAAGTGTATGGCTTCTATGATGAATGCTTTCGGAATATGGAATGC
 QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGlu
 DB 666 AAGTACTTTACAGACTTGTGTTGATTATTGCTCTCACAGCTCTTATAGA
 QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle
 DB 726 TTCTGCCCTACATGGTGGTCTCTCTCCATCATCTGGATCTTTGGATAATGT
 QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyr
 DB 786 GATCGCATACAGAGGTCCGCGCATGAAGGACCTATGTGTGATCTTTTGTG
 QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh
 DB 846 GATGACAGATGGATGGGAAATTTACCAAGGGGTCTGGATACACAT
 QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl
 DB 906 ATTGCACAACTTCAACCATCAAAATGGGCTAAGTCTTATTTCAAGAGC
 QY 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValP
 DB 966 GTATGGAAGGGTTCAATTGTTGTCAGGATAAGAACGTTGTGACAGTGT
 QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGlu
 DB 1026 AACTATTGCTACCGATGCGGAACATGGCTCGCATCTCGAAATTTGGCGA
 QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVa
 DB 1086 CAGAACTTCTCCCAATTCGACCCAGCTCCGCGGAGATTGAGCCGGACAT
 QY 301 ThrProAspTyrPheLeu 306
 DB 1146 ACCCCAGACTACTTTTGG 1163

RESULT 7

US-10-425-114-35277
 ; Sequence 35277, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecule
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improv
 ; FILE REFERENCE: 38-21(53313) B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 35277
 ; LENGTH: 1732
 ; TYPE: DNA
 ; ORGANISM: Zea mays subsp. mexicana

ated With:

FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMPLTBSINTS90H04_FLI
US-10-425-114-35277

Alignment Scores:
Pred. No.: 2,64e-195 Length: 1732
Score: 1518.00 Matches: 272
Percent Similarity: 96.41% Conservative: 23
Best Local Similarity: 88.88% Mismatches: 11
Query Match: 90.90% Indels: 0
DB: 7 Gaps: 0

US-10-764-259-13 (1-306) x US-10-425-114-35277 (1-1732)

```
QY 1 MetProSerTyrAlaAspValaspArgGlnIleGluInLeuSerGluCysIysProLeu 20
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 222 ATGCCGTCGACGCGATCTGGACACCAGATCTCGCAGCTCGCGGATTCGAAAGTTCCTG 281

QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaAArgThrIleLeuValGluLutrp 40
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 282 CGGAGGTGGAGTCAAGACGCTATCGAGAAAGGCAAGCGCATCTCATGGAGGAGTGG 341

QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGlyClnPheHis 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 342 AACGTACAGCCGTCGCTGCCCGCTCACTGTGTGGCGCATCCACGGCCAGTTCTTAC 401

QY 61 AspLeuIleGluLeuPheArgIleGlyGlyIysAlaProAspThrAsnTyrIleuPheMet 80
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 402 GACCTCATCGAGCTCTCGCATCGCGCGCGAGCGGCCAGACACCAACTACTCTTTATG 461

QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 462 GCGGATTACGTGCGCGGTGCTACTCTGTGGAGACTGTGTCTGTGTAGTGCTCTA 521

QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 522 AAGTACGTTATAGACAGATACATATATTTGAGAGGAATCATGAGAGCAGACAAATA 581

QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuAArgLysTyrGlyAsnAlaAsnValTyr 140
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 582 ACTCAAGTGTATGGTCTTATGATGAATGCTTTCGCGAAATATGGAATGCAATGTGTGG 641

QY 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGluHisGluIle 160
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 642 AAGTACTTTACAGACTGTGTTGATTATTTGCCCTCTCACAGCTCTTATAGAAACAGATC 701

QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 702 TTCTGCTACATGGTGGTCTCTCTCCATCAGTGGATACATTGGATTAATTCGCGCCCTT 761

QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyrSerAspPro 200
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 762 GATCGCATACAGAGTCCCATGAAGGACCTATGTGTGATCTTTTGTGGTCTGACCCA 821

QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 822 GATGACCGATGTGGGTGGGAATTTTCCACAGGGGTGCTGGATACACATTTTGGCCAAAGAT 881

QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 882 ATTGCACAACAAATTCACCATACAAATGGGCTTAAGTCTTATTTCAAGGGCCATCACTT 941

QY 241 ValMetGluGlyTyrAsnTyrPcCysGlnAspIysAsnValValThrValPheSerAlaPro 260
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 942 GTAATGGAAGGCTTCAATTTGGTGTGAGGATAAGAAATGTTGTGACTGTGTTCAGCGCGCT 1001

QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1002 AACTACTGTCTACCGATGCGGAACATGGCTGCAATCTCGAAATTTGGCGGAACATGGAT 1061

QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1062 CAGAACTTCTCCAAATTCAGCCAGCTCCACGCGCAAAATTGAGCCGACATGACGCGCAAG 1121
```

```
QY 301 ThrProAspTyrPheLeu 306
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1122 ACACCAGACTACTTTTGG 1139
```

RESULT 8

US-10-437-963-40723
; Sequence 40723, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Mol.
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improv.

; FILE REFERENCE: 38-21(53221)B

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 40723

; LENGTH: 1195

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_44137C.1

US-10-437-963-40723

Alignment Scores:
Pred. No.: 2,9e-194 Length: 1195
Score: 1508.50 Matches: 272
Percent Similarity: 96.09% Conservative: 23
Best Local Similarity: 88.60% Mismatches: 11
Query Match: 90.33% Indels: 1
DB: 7 Gaps: 1

US-10-764-259-13 (1-306) x US-10-437-963-40723 (1-1195)

```
QY 1 MetPro---SerTyrAlaAspValaspArgGlnIleGluInLeuSerGln 19
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ATGCCGTCGTCGACGCGGATCTGGACCGGAGATCTGCGCAGATCGCGCAGCTCGCGGA 60
```

```
QY 20 LeuSerGluLeuGluValIysAsnLeuCysAspGlnAlaAArgThrIleLeu 39
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CTGGCGGAGGGGAGGTGAGGGCGCTGTGCGAGCAGGCGGAGGCCATCTCT 120
```

```
QY 40 TrpAsnValGlnProValLysCysProValThrValCysGlyAspIleHis 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 TGGAAACGTGACGCGGTGCGGTGCGGTACCGTCCGCTACGGTCTCGCGCGCATCCCA 180
```

```
QY 60 HisAspLeuIleGluLeuPheArgIleGlyGlyIysAlaProAspThrAsn 79
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 TACGACCTCATCGAGCTCTTCCGATCCTGCGCGCGCGCGCGCCGACACCAA 240
```

```
QY 80 MetGlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeu 99
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 ATGGCGGACTACGTCGACCGTGGCTACTACTACTCAGTGGAGACTGTTTCGTT 300
```

```
QY 100 LeuIysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGln 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 TTGAAAGTACGCTACAGAGATCGAATTACAATATTGAGAGGAAATCATCA 360
```

```
QY 120 IleThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsn 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 ATCACTCAAGTGTACGGCTTCTACATGAATGCTTGAGAAAGATATGGAAT 420
```

```
QY 140 TrpIysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIle 159
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 421 TGGAAATACTTTACAGACTTGTGTTGATTATTGCTCTCACAGCTCTTAT 480
```

associated With

Qy	160	IlePheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAla	179
Db	481	GTGTTCTGCCTTCACGGTGGCTCTCTCCATCATTTGGATACTTTAGATAACATCCGTGCT	540
Qy	180	LeuAspAtrqIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAsp	199
Db	541	CTTGATCGTATACAGAGGTTCTCATGAGAGCCCATGTGATCTTTTGTGGTCTGAC	600
Qy	200	ProAspAspArgCysGlyTrpGlyIleSerProArgIyAlaGlyTyThrPheGlyGln	219
Db	601	CCAGATGACAGATGCGCGTGGGGAATTTCCAGAGAGCAGCGTTATACATTTGGGCAA	660
Qy	220	AspIleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGln	239
Db	661	GATATCGCTCAACAGTTTAAACATACAATGGTCTATCTCTCACTCAAGGGCACATCAA	720
Qy	240	LeuValMetGluGlyTyTrpAsnTrpCysGlnAspLysAsnValValThrValPheSerAla	259
Db	721	CTTTGTAATGGAGGATTTAATTTGGTGTGCAGACACAAGAAATGTTGTGACGGTCTTCAGTGCA	780
Qy	260	ProAsnTyrCysTyArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMet	279
Db	781	CCAAACTACTGTATTCGTGTGGTAACAATGCGTGCATTCGATTTCTTGAGATTTGGCGAAAACATG	840
Qy	280	AsnArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArg	299
Db	841	GATCAGAACTTCTCCATNTTGTATCCAGCTCTCTGGCNAATTGAAACACAGACACAAACAGC	900
Qy	300	LysThrProAspTyrPheLeu	306
Db	901	AAGACTCCCGACTACTTTTGTG	921

RESULT 9

```

US-10-236-699-25
; Sequence 25, Application US/10236699
; Publication No. US20030150028A1
; GENERAL INFORMATION:
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: CHEN, RUOYING
; APPLICANT: ISHITANI, MANABU
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: COSTA E SILVA, OSWALDO DA
; TITLE OF INVENTION: PROTEIN PHOSPHATASE STRESS-RELATED POLYPEPTIDES AND
; TITLE OF INVENTION: METHODS OF USE IN PLANTS
; FILE REFERENCE: 16313-0161
; CURRENT APPLICATION NUMBER: US/10/236.699
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 60/317,305
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1298
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-236-699-25

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Alignment Scores:		
Pred. No.:	3.3e-194	Length: 1398
Score:	1508.50	Matches: 272
Percent Similarity:	66.09%	Conservative: 23
Best Local Similarity:	88.60%	Mismatches: 11
Query Match:	90.33%	Indels: 1
DB:	6	Gaps: 1

US-10-764-259-13 (1-306) x US-10-236-699-25 (1-1298)

QY 1 MetPro---SerTyrAlaAspValAaspArgGlnileGluGlnLeuSerGluCysLysPro 19
||||| ||||| :::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 173 ATGGCGTGCTGCACGGGATCTGCGCGGAGATCGGCAGCTCGCGAGTCGAACAC 232
QY 20 LeuSerGluLeuGluValLvAsnLeuCyaSpGlnAlaaRathrIleuValGluLu 39

[illegible]

RESULT 10

```

US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Patent No. US2002160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED
; TITLE OF INVENTION: SAME, AND METHOD
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938
; CURRENT FILING DATE: 2001-08-24

```

```
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 705
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-705
```

```
Alignment Scores:
Pred. No.: 2,256-194 Length: 921
Score: 1508.00 Matches: 272
Percent Similarity: 94.44% Conservativeness: 17
Best Local Similarity: 88.89% Mismatches: 17
Query Match: 90.30% Indels: 0
Gaps: 3
```

US-10-764-259-13 (1-306) x US-09-938-842A-705 (1-921)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysIysProLeu 20
DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTGAAGCCGTTA 60
QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaArgThrIleLeuValGluTrp 40
DB 61 GGTGAAGCAGACGTCAGATCCTTTTCGATCAAGCTAAAGCGATCTCTGTGAGGAAT 120
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 121 AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATCGCGCATCATCGCCAGTTTAT 180
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyrLeuPheMet 80
DB 181 GACCTAAATGAGCTATTTTCGATTGGTGAATGCTCTGTACTAAATACCTCTCTCATG 240
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuValAlaLeu 100
DB 241 GGAGATTATGTAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTATTGGTGCATTA 300
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIle 120
DB 301 AAGGTGCGTTACAGGACAGACTTACGATCCTGCGAGGGAATCATGAGAGCGTCAGATT 360
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 361 ACACAACTATGGTTTTTATGACGAATGCTTGAGGAATACGGAATGCAATGTGTGG 420
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
DB 421 AAGTATTTTACGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGATCAGGTT 480
QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 481 TTCTGTGTGCATGGAGCGCTTTTCACTCTCTGGAATCTCTTGAACAATATCCGAAGCTTG 540
QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 541 GATCGAATACAGAGGTTCCACAGAGGACCAATGTGCGATCTACTCTGGTCTGATCCC 600
QY 201 AspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
DB 601 GACGATCGTTGTGGATGGGAATATCTCCTCGTGTGCTGGTTACACGTTTTCGACAGGAC 660
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
DB 661 ATTGCTACTCAGTTTAAATCATAACTAGGACTGAGTCTGATCTCAAGAGCGCATCACTT 720
QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
```

```
DB 721 GTAATGGAGGCTATATATTGGTGTCTAGGAAAGACGTAGTGCACAGTGT 780
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaIleMetGluIleAspGly 280
DB 781 AACTACTGTTACAGATGTGGAAACATGGCCCAATTTCTTGAGATTGGAGAJ 840
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal 300
DB 841 CAGAACTTCTTCAATTCGATCCAGCACCTAGACAAAGTCGAACCCGATAC 900
QY 301 ThrProAspTyrPheLeu 306
DB 901 ACCCTGATTAATTTTTTG 918
```

RESULT 11

US-09-938-842A-705
; Sequence 705, Application US/09938842A
; Publication No. US20040009476A9

GENERAL INFORMATION:

; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENES
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 705
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-705

Alignment Scores:
Pred. No.: 2,256-194 Length: 921
Score: 1508.00 Matches: 272
Percent Similarity: 94.44% Conservativeness: 17
Best Local Similarity: 88.89% Mismatches: 17
Query Match: 90.30% Indels: 0
Gaps: 3

US-10-764-259-13 (1-306) x US-09-938-842A-705 (1-921)

```
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCys 20
DB 1 ATGCCGTTAAACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGT 60
QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal 40
DB 61 GGTGAAGCAGACGTCAGATCCTTTTCGATCAAGCTAAAGCGATTTCTGT 120
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60
DB 121 AATGTTCAACCGGTTAAGTGTCCGGTTACGGTATCGCGCATATCCATGG 180
QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTyr 80
DB 181 GACCTAAATGAGCTATTTTCGATTGGTGTATGCTGTCTCTGATCTAATTA 240
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 241 GGAGATTATGTAGATCGGTGCTACTATTCTGTAGAAACAGTCTCTCTATT 300
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe 120
```

Db 301 AAGTGGCGTTACAGGACAGACTTACGATCCTCGAGGGAATCATGAGACCGCTCAGATT 360
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaSerValTrp 140
Db 361 ACACAGCTCATGGTTTATCAGCAATGCTTGAGAAATACGGAATGCAAAATGTGTGG 420
Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuLeuLeuHisGluLe 160
Db 421 AAGTATTTTACGACCTTTTCGATTATCTCCCTCTTACAGCACTCATAGAGAGTCAGGTT 480
Qy 161 PheCysLeuHisGlyCysLeuSerProSerLeuAspThrLeuAspHisLeuArgAlaLeu 180
Db 481 TTCTGTTGTCATGGAGCGCTTTTACCTTCTCTGSGATCTCTTGCACAATATCCGAAGCTTG 540
Qy 181 AspArgGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
Db 541 GATCGAATACAGAGGTTCCACAGAGGACCAATGTGGGATCTACTCTGGTCTGATCCC 600
Qy 201 AspAspArgCysGlyTrpGlyLeuSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
Db 601 GACGATCGTTGGATGGGAATATCTCTCTGCTGGTGTGCTTACACGTTTGCACAGGAC 660
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db 661 ATTGCTACTCAGTTTAATCATAACTAATGAGTCTGATCTCAAGAGCGCATCAACTT 720
Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 721 GTAATGGAGGCTTAATTTGGTGTGAGGAAGACGTAGTACAGTGTTTAGTGACCG 780
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsn 280
Db 781 AACTACTGTTACAGATGTGGAAACATGCGCGCAATCTTTGAGATGGAGAAAGATGGAA 840
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 841 CAGAACTTCTCTTCAATTCGATCCAGCACCTAGACAAAGTCGAACCGGATACACGCGCAAG 900
Qy 301 ThrProAspTyrPheLeu 306
Db 901 ACCCTGATATTTTGG 918

RESULT 12
US-09-938-842A-571
; Sequence 571, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 571
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-571
Alignment Scores:
Pred. No.: 1.34e-192 Length: 924
Score: 1495.00 Matches: 268
Percent Similarity: 95.41% Conservative: 23

Best Local Similarity: 87.87% Mismatches: 14
Query Match: 89.52% Indels: 0
Db: 3 Gaps: 0
US-10-764-259-13 (1-306) x US-09-938-842A-571 (1-924)
Qy 2 ProSerTyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysGly 21
Db 7 CCGCGACCGGAGATATCGATCGTCAGATCGAGCAGCTTATGGAGGTAA 66
Qy 22 GluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValG 41
Db 67 GAAACGGAGGTGAAGATGTTGTGTGAGCACCAAGACGATTTCTTTGTGA 126
Qy 42 ValGlnProValLysCysProValThrValCysGlyAspIleHisGlyG 61
Db 127 GTTCAACCGGTTAATGTCCGGTTACCGTCTGCGGTGATATCCAGCGCA 186
Qy 62 LeuIleGluLeuPheArgGlyGlyCysAlaProAspThrAsnTyrLe 81
Db 187 CTAATCGAGCTTTTCTGATCGTGGTGTCTCTCTGATACTAATATCT 246
Qy 82 AspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuVa 101
Db 247 GATTATGTTGATCGAGGGTATTATTCTGTGAGACAGTCTCACCTTTGGT 306
Qy 102 ValArgTyrArgAspArgGlyLeuThrIleLeuArgGlyAsnHisGluSerAr 121
Db 307 GTTCTTACAGAGATAGACTTACTATCTTAAGAGGGAATCATGAAGCGG 366
Qy 122 GlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAs 141
Db 367 CAAGTGTATGGTTTATGATGAATGTTTGGAGAAATATGGAATGTCTAA 426
Qy 142 TyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHi 161
Db 427 CACTTCACTGATCTTTTGTGATTATCTTCCACTTACAGCTCTTATTGAGAG 486
Qy 162 CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleAr 181
Db 487 TGTTTACATGAGGACTTTTCACTTCTTTAGATACACTTGACATCCG 546
Qy 182 ArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTrpSe 201
Db 547 CGAATTCAAGAGGTTCCACATGAAGGACCAATGTGTGATCTCTTATGGTC 606
Qy 202 AspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGl 221
Db 607 GACCGATCGGTTGGGAAATATCTCTCTGCTGCGAGCTACACTTTCCG 666
Qy 222 AlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHi 241
Db 667 GCTACTCAGTTTACCAACCAATGGACTCTCTCTGATTTCAAGAGCACA 726
Qy 242 MetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSe 261
Db 727 ATGGAAGGTTTAAATGTTGTCGCAAGAAAGAACGTTGTGACTGTATTAG 786
Qy 262 TyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluTh 281
Db 787 TATTGCTACCGTTTGTGGCAACATGCTCGGATTTCTAGAGATCGGTGAGAA 846
Qy 282 SerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValTh 301
Db 847 AATTTCCTTCAAGTTGATCCAGTCCAGCTCCAGTCAAGTCCGAACCCGAACCA 906
Qy 302 ProAspTyrPheLeu 306
Db 907 CCAGATTATTTTGG 921

RESULT 13
US-09-938-842A-571
; Sequence 571, Application US/09938842A

Qy	81	GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu	100
Db	432	GGCCACTACGTCGATCGGGCTATTATTACGTTGAAACAGTTTCTCTCTTAGTGGCTTG	491
Qy	101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle	120
Db	492	AAAGTCGGTTACAGAGATAGAAATTACAATACTTAGAGGAAATCATGAGCGACAGCAATC	551
Qy	121	ThrGlnValTyrGlyPheTyrAspGluCysLeuArgIleTyrGlyAsnAlaAsnValTrp	140
Db	552	ACTCAAGTATATGGCTTCTATGATGAATGCTTAAGAAAAATATGAAATGCAAAATGCTCTG	611
Qy	141	LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle	160
Db	612	AAGTATTTTACAGACTTGTGTGATTTTGTGCTCTCACAGCTCTATAGAAAAATCAGGTC	671
Qy	161	PheCysLeuHisGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu	180
Db	672	TTCTGTCTTCATGCTGGGCTCTCTCCGTCATTTGGACACATTTGGATAATATTCGTTCTTT	731
Qy	181	AspArgIleGlnGluValPro-HisGluGlyProMetCysAspLeuLeuTrpSerAspPr	200
Db	732	GATCGCTACAGGAGGTTCTCTCCATGAGGACCCATGTGTGATCTTTGTGCTGCACCC	791
Qy	200	oAspAspArgCysGlyTrpGlyIleSerProArgGlyValaglyTyrThrPheGlyGlnAs	220
Db	792	AGATGACCGATGTGGATGGGGAATTTACCAGAGGAGCAGGTTACACATTTGGCGCAAGA	851
Qy	220	pIleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaargAlaHisGlnLe	240
Db	852	CATTGGCGCAGCAGTTC AACATCAAAATGGTCTTTCTCTCATTTCAAGGGCCATCAACT	911
Qy	240	uValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAlaPr	260
Db	912	TGTAATGGAAAGGATTAATTTAGTGGTCCAGGATAAGAAATGTAGTCACAGCTTTCAGTGGGCC	971
Qy	260	oAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAs	280
Db	972	TAATTACTGTTTACCCTGTGGTAAATCATGGCTGCTATTCTTGAAATCGGGGAAAAATGGA	1031
Qy	280	nArgSerPheLeuGlnPheGluProAlaProArg-GlnSerGluProAspValThrArgL	300
Db	1032	CCAGAACTTCTTCAATTC AACCCCGCACCTCGGGCAAAATTGACCCAGACACAACTGC	1091
Qy	300	ysThrProAspTyrPheLeu 306	
Db	1092	AAACCCAGACTACTTTCTG 1111	

RESULT 15

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US-10-425-115-160546
; Sequence 160546, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J.
; APPLICANT: La Rosa, David K.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 160546
; LENGTH: 1759
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_77998C.1
US-10-425-115-160546

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Alignment Scores:

Pred. No.:	7.6e-187	Length:	1759
Score:	1456.00	Matches:	272
Percent Similarity:	75.45%	Conservative:	23
Best Local Similarity:	69.57%	Mismatches:	11
Query Match:	87.19%	Indels:	85
DB:	8	Gaps:	1
US-10-764-259-13 (1-306) x US-10-425-115-160546 (1-1759)			
Qy	1	MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCy	eu 20
Db	327	ATGCCATCGCAGCGGATCTGGACCGCCACAGATCTCGCAGCTGCGGATTC	TC 386
Qy	21	SerGluLeuGluValIysAsnLeuCysAspGlnAlaAargThrIleLeuVa	rp 40
Db	387	CCTGAGCGGAGGTCAAACGCTATCGCAGCAGCGCAAGCGCATCTCAT	3G 446
Qy	41	AsnValGlnProValIysCysProValThrValCysGlyAspIleHisG1	1e 60
Db	447	AACGTGAGCCCGTGGCTGCCCGTCACTGTCTGGCGCAGATCCACGG	AC 506
Qy	61	AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy	et 80
Db	507	GACCTCATCAGCTCTTCGCATCGGTGGCGCGCCGACACCAACTA	TC 566
Qy	81	GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe	eu 100
Db	567	GGCGACTACGTCCACCGTGGCTACTACTCAGTGGAGACTGTGTTCCTATT	TA 626
Qy	101	LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe	1e 120
Db	627	AAAGTAGCTTATAGACAGAGAAATCACAATATTGAGAGGAAATCATGAGAG	TA 686
Qy	121	ThrGlnVal-----	-- 123
Db	687	ACTCAAGTGTATGGCTTCTATGATGAATGCTTGGCGAAATATGGAATGC	CG 746
Qy	123	-----	-- 123
Db	747	AAGTACTTTACAGACTTGGTTGATTATTTGTTGATTTCAGATGGAAAAAT	CT 806
Qy	123	-----	-- 123
Db	807	ACTGTAGATTACAGATGGGTAATACTGACAGGATATAGAATTCGAACTTC	3A 866
Qy	123	-----	-- 123
Db	867	TCACTTGGTCTGTTTTTCTAACTGTAGGACATTATAGTGCATGTTTTATCA	CC 926
Qy	124	-----TyrGlyPheTyrAspGluCysLeuArgI	As 136
Db	927	CTTGACAAACATTTCCACAGGTATGGCTTCTATGATGAATGCTTCGCGA	AA 986
Qy	136	nAlaAsnValTrpLysTyrPheThrAspLeuPheAspTyrLeuProLeuI	1I 156
Db	987	TGCAAATGTGGAAGTACTTTACACACTTGTTGATTATTTGCCCTCTCA	AT 1046
Qy	156	eGluHisGluIlePheCysLeuHisGlyGlyLeuSerProSerLeuAspT	Hi 176
Db	1047	AGAAAATTCAGATCTTCTGCCCTACATGGTGGTCTCTCTCCATCACTGGATA	AA 1106
Qy	176	sIleArgAlaLeuAspArgIleGlnGluValProHisGluGlyProMetC	Le 196
Db	1107	TGTCGGCTCCCTTGATCGCATACAAGAGGTCCCGCATGAAGGACCTPATGI	TT 1166
Qy	196	uTrpSerAspProAspAspArgCysGlyTrpGlyIleSerProArgGlyA	Th 216
Db	1167	GTGGTCTGACCCGGATGACAGATGTGATGGGGAATTTTACCACAGGGGTTC	AC 1226
Qy	216	rPheGlyGlnAspIleAlaGluGlnPheAsnHisThrAsnGlyLeuSerI	Ar 236
Db	1227	ATTTGGCCAAATATTGCAACAATTTCAACCATACAATGGGTAAAGTTC	AG 1286

Qy	236	gAlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrVa	256
Db	1287	AGCTCATCAACTTGTAAATGGAAGGGTTCAATTGGTGCCAGGATAAGAACGTTGTGACAGT	1346
Qy	256	lPheSerAlaProAsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAs	276
Db	1347	GTTTCAGCGCGCTAACTATTGCTACCGATGCGGAAACATGGCTGCGATCCTCGAAATTGG	1406
Qy	276	pGluThrMetAsnArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAs	296
Db	1407	CGAGAACATGGATCAGAACTTCCTCCAATTCGACCCAGCTCCGCGGCAGATTGAGCCGGA	1466
Qy	296	pValThrArgLysThrProAspTyrPheIeu	306
Db	1467	CATGACGCGCAAGACCCAGACTACTTTTGT	1497

Search completed: December 9, 2005, 13:12:22
Job time : 833 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:37:52 ; Search time 248 Seconds
(without alignments)
461.288 Million cell updates/sec

Title: US-10-764-259-13
Perfect score: 1670
Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPRQSPDVTRKTPDYFL 306

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO spool p/US10764259/runat_05122005_094549_7109/app_query.fasta.1.455
-DB=PublishedApplications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=2000000000 -USER=US10764259 @CNC 1.184 @runat_05122005_094549_7109
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Match	Length	Description
1	1411	84.5	1541	US-10-909-125-814 Sequence 814, App
2	111.5	6.7	3342	US-10-750-185-59362 Sequence 59362, A
3	107.5	6.4	3964	US-10-750-185-37665 Sequence 37665, A
4	96.5	5.8	1147	US-10-750-185-37096 Sequence 37096, A
5	93	5.6	1861	US-10-750-185-62270 Sequence 62270, A
6	89	5.3	728	US-10-750-185-37667 Sequence 37667, A
7	87.5	5.2	828	US-10-467-657-2501 Sequence 2501, Ap
8	87.5	5.2	963	US-10-467-657-2503 Sequence 2503, Ap

c	9	87	5.2	491	6	US-10-750-185-3553	Sequ
	10	87	5.2	753	7	US-11-135-855-18	Appl
	11	87	5.2	163162	7	US-11-121-086-66	Appl
c	12	86	5.1	2348	6	US-10-750-185-33466	66, A
	13	82.5	4.9	2401	6	US-10-955-054A-137	Sequ
	14	82.5	4.9	2740	6	US-10-955-054A-101	Sequ
	15	82.5	4.9	191797	7	US-11-121-086-13	Sequ
	16	82	4.9	157224	7	US-11-112-908-51	Appl
	17	82	4.9	161726	7	US-11-112-908-48	Appl
	18	82	4.9	161726	7	US-11-112-908-52	Appl
	19	82	4.9	170189	7	US-11-112-908-50	Appl
	20	81.5	4.9	1272	6	US-10-467-657-2677	7, Ap
c	21	81.5	4.9	3242	6	US-10-750-185-35660	60, A
	22	80	4.8	2107	6	US-10-750-185-44725	25, A
	23	80	4.8	3065	6	US-10-793-626-3730	Sequ
c	24	78	4.7	153142	7	US-11-121-086-27	Appl
	25	77	4.6	2530	6	US-10-821-234-276	Sequ
c	26	77	4.6	3242	6	US-10-793-626-3733	Sequ
	27	76.5	4.6	1878	6	US-10-467-657-6425	Sequ
	28	76.5	4.6	1878	6	US-10-467-657-7617	Sequ
	29	76.5	4.6	2091	7	US-11-029-003-9	Appl
c	30	76.5	4.6	3730	6	US-10-485-517-116	Sequ
	31	76	4.6	792	6	US-10-467-657-6939	9, Ap
	32	76	4.6	963	6	US-10-750-185-46644	44, A
	33	75.5	4.5	2031	7	US-11-058-727-51	Sequ
	34	75.5	4.5	2031	7	US-11-058-727-83	Appl
	35	75.5	4.5	2031	7	US-11-108-389-51	Sequ
	36	75.5	4.5	2031	7	US-11-108-389-83	Appl
c	37	74.5	4.5	1157	6	US-10-750-185-34749	49, A
	38	74.5	4.5	1380	6	US-10-793-626-1245	Sequ
	39	74.5	4.5	1380	6	US-10-793-626-2553	5, Ap
	40	74.5	4.5	1534	6	US-10-750-185-38375	3, Ap
	41	74.5	4.5	2998	6	US-10-793-626-3506	75, A
c	42	74.5	4.5	3527	6	US-10-793-626-3890	6, Ap
	43	74	4.4	1557	6	US-10-793-626-505	0, Ap
c	44	74	4.4	1693	6	US-10-750-185-50007	Sequ
	45	74	4.4	3202	6	US-10-793-626-3386	07, A

ALIGNMENTS

RESULT 1

US-10-909-125-814
; Sequence 814, Application US/10909125
; Publication No. US20050261218A1
; GENERAL INFORMATION:
; APPLICANT: Esau, Christine
; APPLICANT: Lollo, Bridget
; APPLICANT: Bennett, C. Frank
; APPLICANT: Freier, Susan M.
; APPLICANT: Griffey, Richard H.
; APPLICANT: Baker, Brenda F.
; APPLICANT: Vickers, Timothy
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Koller, Erich
; APPLICANT: Swayze, Eric
; APPLICANT: Jain, Ravi
; APPLICANT: Bhat, Balkrishen
; APPLICANT: Peralta, Eige
; TITLE OF INVENTION: Oligomeric Compounds And Compositions For
; FILE OF INVENTION: Of Small Non-Coding RNAs
; FILE REFERENCE: IGIS0080-100 (CORE0016US)
; CURRENT APPLICATION NUMBER: US/10/909,125
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US 60/492,056
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 60/516,303
; PRIOR FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/531,596
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/562,417
; PRIOR FILING DATE: 2004-04-14
; NUMBER OF SEQ ID NOS: 2184

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 814

; LENGTH: 1541

; TYPE: DNA

; ORGANISM: H. sapiens

US-10-909-125-814

Alignment Scores:

Pred. No.: 1.5e-171 Length: 1541
Score: 1411.00 Matches: 248
Percent Similarity: 93.69% Conservative: 34
Best Local Similarity: 82.33% Mismatches: 19
Query Match: 84.49% Indels: 0
DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-909-125-814 (1-1541)

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Qy      6 AspValAspArgGlnIleGlnLeuSerGluCysLysProLeuSerGluLeuGluVal 25
Db      46 GAGCTGGACCAAGTGGGTGAGCAGCTGAACGAGTGAAGCTGAACGAGAACCAAGTG 105

Qy     26 LysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrpAsnValGlnProVal 45
Db     106 CGGACGCTGTCGACAGCAAGCAAAATTTTAAACAAAGAAATCAATGTGCAAGAGTT 165

Qy     46 LysCysProValThrValCysGlyAspIleHisGlyGlnPheHisAspLeuGluLeu 65
Db     166 CGTTCCTCTGTTACTGTCTGTGGAGATGTCATGCTCAATTTTCATGATCTTTATGGAATC 225

Qy     66 PheArgIleGlyGlyValAspAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAsp 85
Db     226 TTTAGAAATGGTGGAAATACCCGAGATCAAACTACTTATTCATGGGTGACTATGTAGAC 285

Qy     86 ArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArg 105
Db     286 AGAGATATATTTCAGTGGAGACTGTGACTCTTCTGTAGCATTAAGAGTGGGTATCA 345

Qy    106 AspArgIleThrIleLeuArgGlyAsnHisGlySerArgGlnIleThrGlnValTyrGly 125
Db    346 GAACGCATTACAAATATTGAGAGGAATCAGCAAGCCGACAAATTTACCAAGTATATGGC 405

Qy    126 PheTyrAspGluCysLeuArgIleValTyrGlyAsnAlaAsnValTrpLysTyrPheThrAsp 145
Db    406 TTTTATGATGAATGTCGGAAGATATGGGAATGCCAAGCTTGGAAATATTTTACAGAT 465

Qy    146 LeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGly 165
Db    466 CTCCTTTGATTATCTCCACTTACAGCTTTAGTAGATGGACAGATATTTCTGCCTCATG 525

Qy    166 GlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGlu 185
Db    526 GGCCTCTCTCCATCCATAGACACACTGGATCATATATAAGAGCCCTGGATCGTTTACAGAA 585

Qy    186 ValProHisGluGlyProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGly 205
Db    586 GTTCACATAGAGGCCCAATGTTGATCTGTTATGGTCAGATCCAGATGATCGTGGTGA 645

Qy    206 TrpGlyIleSerProArgGlyValaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPhe 225
Db    646 TGGGGTATTTCACACCGTGGTCTGGCTACACATTTGGCAAGACATTTCTGAAACCTTT 705

Qy    226 AsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyr 245
Db    706 AACCATGCAATGGTGTCTACACATGGTTTCTCGTGGCCACCAAGCTTGTAAATGGAGGATAC 765

Qy    246 AsnTyrCysGlnAspLysAsnValValThrValPheSerAlaProAsnTyrCysTyrArg 265
Db    766 AATTGGTGTGATGTCGAATGTTGTTTACCATTTTCAGTGCACCAATTTACTGTTATCGT 825

Qy    266 CysGlyAsnMetAlaAlaIleMetGluLeuAspGluThrMetAsnArgSerPheLeuGln 285
Db    826 TGTGGGAACAGGCTGCTATCATCGAAATTAGATGACACTTTTAAATAATTTCTCTTCAA 885
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Qy      286 PheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 305
Db     886 TTTGACCGCGCGCTCGTGGTGGAGCCTCATGTTACACGGCGCACCCC 945

Qy     306 Leu 306
Db     946 CTA 948

RESULT 2
US-10-750-185-59362
; Sequence 59362, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 59362
; LENGTH: 3342
; TYPE: DNA
; ORGANISM: Bovine 19866880635842
US-10-750-185-59362

Alignment Scores:
Pred. No.: 0.00451 Length: 3342
Score: 111.50 Matches: 64
Percent Similarity: 44.29% Conservative: 29
Best Local Similarity: 30.48% Mismatches: 80
Query Match: 6.68% Indels: 39
DB: 6 Gaps: 8

US-10-764-259-13 (1-306) x US-10-750-185-59362 (1-3342)

Qy      56 HisGlyGlnPheHisAspLeuIleGluLeuPheArgIle-GlyGlyLysA 75
Db     1453 CACGGTCAATTTCTAGATGCTACCACGTCTTTAGAACTGAGGGGAAAGA 1512

Qy      75 rAsnTyrLeuPheMetGlyAsp-----TyrV; 87
Db     1513 GAATTTATGTACATGTGGGTAATATAGAGGCTTCTCTGTAGCTCAGCTGG 1572

Qy      87 yTyr-Tyr-SerValGluThrVal-----SerLeuL 100
Db     1573 GCCTGTAACACAGGAACCTGGTAAGATGAAGACAGCATAGACTGTGGC 1632

Qy     100 uLysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGly 120
Db     1633 TAGAGGGTCAGAAATTAGAGACTCTAACACAGCATTTGAAAGGAAGCAATGAAG 1691

Qy     120 eThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnA 140
Db     1692 TAACCAAGTGTGACACTTTTATGATGGCTGT---TGAGAGTAAGACATG 1748

Qy     140 pLysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleG 160
Db     1749 GGAAGTATTACACACATGATGTGTTCTTCTCTCTGGGCACTGGTC- 1797

Qy     160 ePheCysLeuHisGly-GlyLeuSerProSerLeuAspThr-----Leu 178
Db     1798 ----TGT-----GGGTAACTCTCACTCTGTTTCACAGACACACCTCCCTG 1847

Qy     178 rgAlaLeuAspArgIleGlnGluValProHisGluGlyProMetCysAsp 197
```


Qy 59 PheHisAspLeuLeuGluLeuPheArgTleGlyGlyLysAlaProAspThrAsnTyrLeu 78
 Db 1636 TTTTATGACCTTTGTGAACCTGTTCAAGACTGGAGGTCAGGTTCTCTGACACAAACTACATA 1695

Qy 79 PheMet 80
 Db 1696 TTTATG 1701

RESULT 6

US-10-750-185-37667
 ; Sequence 37667, Application US/10750185
 ; Publication No. US20050260603A1

GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MW1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37667
 ; LENGTH: 728

; TYPE: DNA

; ORGANISM: Bovine 198668080838231

US-10-750-185-37667

Alignment Scores:
 Pred. No.: 0.36 Length: 728
 Score: 89.00 Matches: 15
 Percent Similarity: 80.95% Conservative: 2
 Best Local Similarity: 71.43% Mismatches: 4
 Query Match: 5.33% Indels: 0
 DB: 6 Gaps: 0

US-10-764-259-13 (1-306) x US-10-750-185-37667 (1-728)

Qy 180 LeuAspArgIleGlnGluValProHisGluGlyProMetCysAspLeuTrpSerAsp 199
 Db 650 TTAGACCGATTCAAGAACCACTGCTTATGGACCTATGTGTGATATCTGTGGTCAGAC 709

Qy 200 Pro 200

Db 710 CCG 712

RESULT 7

US-10-467-657-2501

; Sequence 2501, Application US/10467657
 ; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: SeqWing99, version 1.04

; SEQ ID NO 2501

; LENGTH: 828

; TYPE: DNA
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-2501

Alignment Scores:

Pred. No.: 0.684 Length: 828
 Score: 87.50 Matches: 52
 Percent Similarity: 35.58% Conservative: 22
 Best Local Similarity: 25.00% Mismatches: 69
 Query Match: 5.24% Indels: 65
 DB: 6 Gaps: 10

US-10-764-259-13 (1-306) x US-10-467-657-2501 (1-828)

Qy 53 GlyAspIleHisGlyGlnPheHisAspLeuLeuGluLeuPhe---ArgIle 70
 Db 19 GGCACATCCAAGGCTGTTTCGACGAACTGACCGCGCTGCTCGGCAAAAT 78
 Qy 71 LysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArgIle 90
 Db 79 CACGGCACGGACACCCTCTGGCTG---ACGGCGACATCGTCAACCGCGG 135
 Qy 91 ValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAspAr 110
 Db 136 CTCGAACGCTGCAATTCTGTC-----ATCGGCGACGAAACAG 183
 Qy 111 LeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTy 130
 Db 184 GTCCTCGGCAACCAACGAC----- 201
 Qy 131 LeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPh 150
 Db 202 ----- 204
 Qy 151 ProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGlyLe 170
 Db 205 TACCTGCTCGCC-----GTCGGCTGCGCGAAGGCGCGCT 249
 Qy 171 LeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluValPr 190
 Db 250 ---GACACA-----ATCGAACCCATATACTCAAAACACC 288
 Qy 191 ProMetCysAspLeuLeuTrpSerAspProAspAspArgCysGlyTrpGl 210
 Db 289 AAAATGCTCGACTCGCTCGCGCGCAACCG-----CT 330
 Qy 211 ArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAsnHi 230
 Db 331 GAGGCGCGCGCTGATGATACACCGCGCATCTCGCGCAATGGCGC-- 378
 Qy 231 LeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsnTr 250
 Db 379 -----ATAGCCAAAGCCGAATCGCTCGCGGAGAGCGCAAGCGGA 429

RESULT 8

US-10-467-657-2503/c

; Sequence 2503, Application US/10467657

; Publication No. US20050260581A1

GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8

```
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2503
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2503

Alignment Scores:
Pred. No.: 0.861 Length: 963
Score: 87.50 Matches: 52
Percent Similarity: 35.58% Conservative: 22
Best Local Similarity: 25.00% Mismatches: 69
Query Match: 5.24% Indels: 65
DB: 6 Gaps: 10

US-10-764-259-13 (1-306) x US-10-467-657-2503 (1-963)
Qy 53 GlyAspIleHisGlyGlnPheHisAspLeuIleGluLeuPhe---ArgIleGly---Gly 70
Db 774 GGCAGATCCAAAGGCTGTTTCAGCAACTGACCGCGCTGCTCGGCAAAATCGGCTTCAC 715
Qy 71 LysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArgGlyTyrTyrSer 90
Db 714 CACGGCAGCGACACCCCTCTGGCTG---ACGGGCGACATCGTCAACCGCGCGCGCAAAATCC 658
Qy 91 ValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAspArgIleThrIle 110
Db 657 CTCGAAGCGTGCATTCCTGC-----ATCCGGCAGCAAAACAGCGGTGCAAAATC 610
Qy 111 LeuArgGlyAsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCys 130
Db 609 GTCCCTCGCAACACGAC-----592
Qy 131 LeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPheAspTyrLeu 150
Db 591 -----CTG 589
Qy 151 ProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGlyLeuSerProSer 170
Db 588 TACCTGCTCGCC-----GTGCGCTGCGCGGAGGCGCGCTCAAAAGCGAGC 544
Qy 171 LeuAspThrLeuAspHisIleArgAlaLeuAspArgIleGlnGluValProHisGluGly 190
Db 543 ---GACACA-----ATCGAACCCATCTCAACACCCCGCGCGCGGA 505
Qy 191 ProMetCysAspLeuLeuTrpSerAspProAspArgCysGlyTrpGlyIleSerPro 210
Db 504 AAAATGCTCGACTGGCTGCGCGCGCAACCG-----CTTTTGATACGC 463
Qy 211 ArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluGlnPheAsnHisThrAsnGly 230
Db 462 GAGGCGCGCGCGTGATGATACACCGCGCATCTCGCGCAATGGCG-----415
Qy 231 LeuSerLeuValAlaArgAlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAsp 250
Db 414 -----ATAGCAAAAGCCGAATCGCTCGCGGAGAGCGGAGCGAAATCGCGCGC 364
Qy 251 LysAsnValValThrValPheSer 258
Db 363 AAAAAATACGTCAAAATCTCTCTCC 340

RESULT 9
US-10-750-185-3553/c
; Sequence 3553, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3553
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Bovine MMBT13351
US-10-750-185-3553

Alignment Scores:
Pred. No.: 0.359 Length: 491
Score: 87.00 Matches: 19
Percent Similarity: 54.55% Conservative: 11
Best Local Similarity: 34.55% Mismatches: 23
Query Match: 5.21% Indels: 2
DB: 6 Gaps: 1

US-10-764-259-13 (1-306) x US-10-750-185-3553 (1-491)
Qy 94 ValSerLeuLeuValAlaLeuLysValArgTyrArgAspArgIleThrIle 113
Db 490 GTCTTATATTATGGTCTCGCAAGATCTGTATCCAGTACATTATTCT 431
Qy 114 AsnHisGluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCys 133
Db 430 AACCATGAATCGACACACCTTACTGAATATTTTACCTTTTAAGCAGGAATG 477
Qy 134 TyrGlyAsnAlaAsnValTrpLysTyrPheThrAspLeuPheAsp 148
Db 376 TACTGCCATGAGAACTATTTTCACTTCTCAGGGTTCTTTTAGAG 332

RESULT 10
US-11-135-855-18
; Sequence 18, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 753
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-18

Alignment Scores:
Pred. No.: 0.687 Length: 753
Score: 87.00 Matches: 49
Percent Similarity: 35.14% Conservative: 29
Best Local Similarity: 22.07% Mismatches: 80
Query Match: 5.21% Indels: 64
DB: 7 Gaps: 11
```



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; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 53466
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine
US-10-750-185-53466

Alignment Scores:
Pred. No.: 5.22 Length: 2348
Score: 86.00 Matches: 40
Percent Similarity: 39.07% Conservative: 19
Best Local Similarity: 26.49% Mismatches: 61
Query Match: 5.15% Indels: 31
DB: Gaps: 7

US-10-764-259-13 (1-306) x US-10-750-185-53466 (1-2348)

QY 97 LeuValAlaLeuLysValArgTyrArgAspArg-----lleThrIleLeu 111
|||:::||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 576 CTTTATTGTTAGAAAAAAGATACAGGCNAAGAAATGAAGAATGACTTTGTACCATCATC 517
|||:::||||:::||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 112 ArgGlyAsnHisGluSerArgGln-IleThrGlnValTyrGlyPhe----- 126
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 -----TGNAGCAATAGCATTTGACTAGTAATCTACTCATCTCTCAGCCCTGGTC 466
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 ----TyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLys----- 141
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 465 CTAGTTAGTCCCTGCTCTTTTGGCAAGGGCTCTCAGAGTGTACGAAGCGCATCTCACA 406
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 142 -TyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePh 161
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 405 TGTACTAACAGATTTTTTTTCATGCTTTCCCAAGGCTCTGCGAGTTGCTTATGAGATCAT 346
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 161 e--CysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIle----- 177
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 345 GCAGACGGTGCATCCCGATGGCTCTGCNAATCTTCATCTTTGGATGACATCTACTATT 286
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 178 -----ArgAlaLeuAspArgIleGlnGluValProHisGluGlyProMetCysAs 194
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 285 TGGAGGCCAAATGCCACACACCAGATTGCTATTATTTCTCAGAACCTCGAACTCGCGA 226
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 pLeuLeuTrpSerAspProAspAspArgCysGly-----TrpGlyIleSe 209
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 225 TGAATATCCCATGGCAACCTGGAGATATCATTTGGCGTGGCTGGAAATCACTGGGATGCTA 166
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 209 rProArgGlyAlaGlyTyrThrPheGlyGln 219
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 165 TTCTAAAGGTGTCAACAGAAAACTGGGAAGG 135
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-955-054A-137
; Sequence 137, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:8800S
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 137
; LENGTH: 2401

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<hr/>					
:	TYPE: DNA				
:	ORGANISM: Homo sapiens				
<hr/>					
US-10-955-054A-137					
<hr/>					
Alignment Scores:					
Pred. No.:	15.3	Length:	2401		
Score:	82.50	Matches:	66		
Percent Similarity:	37.12%	Conservative:	68		
Best Local Similarity:	18.84%	Mismatches:	156		
Query Match:	4.94%	Indels:	72		
DB:	6	Gaps:	13		
<hr/>					
US-10-764-259-13 (1-306) x US-10-955-054A-137 (1-2401)					
Qy	4	TyrAlaAspValAspArgGlnIleGluLeuSerGluCysLysProLeu			
Dd	1306	TATGCCATGGCTCCCGGAGCGTCTTCCTCTGTAA-GAATCAACCCGTCT	:		
Qy	24	GluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGlu-	: : :		
Dd	1365	GGGCCTCGGAAGTCTATGTGACATTCTTCGAGATCTCAATGGGAAGCTGT	: :		
Qy	43	nProValLysCysProValThrValCysGlyAsp-----	: : :		
Dd	1425	CAACAAGAAGCCCAAGCTGCGCGTGCTGGAGAGCGGCAAGCAACAGGTGTC	: :		
Qy	56	sGlyGlnPheHis-----AspLeuIleGluLeuPheA	: :		
Dd	1485	GCTCCAGGAGCATCTGGTTAACTCTGTGATGATCTCATCAAGATGCTCTC	: :		
Qy	70	yLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArg-	:: :: ::		
Dd	1545	CGCCTGCAGAACCTCTGGCGAGACATTTGCCAACTCCAATTCCTCCCGCT	: :		
Qy	90	rValGluThrValSerLeuLeuValAlaLeuLysValArgTyrArgAspA	: :		
Dd	1605	CTTCCAA-----ATTATTCTCGAGCTAAAGGGAGAAATGCATGGCA	: :		
Qy	110	e-----LeuArgGlyAsnHis-----	: :		
Dd	1656	GGTAGACTCTGGCAGGGAATGCCAGCGGCAGACACTTCCAGTGCCTGACC	: :		
Qy	116	----GluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCysl	: :		
Dd	1716	CATGGAGCGGCAGAAATCAACAAGAGTCTCTTAGCCCTGAAGGAGTGCA	: :		
Qy	134	rGlyAsnAlaAsnValTrpLysTyrPheThrAsp-----LeuPheAspI	: :		
Dd	1776	GGGACAGAACAGGCTCACACCCCCTCCGCTGAGAGCAAGCTGACACAGG	: :		
Qy	152	uThrAlaLeuIleGluHisGluIlePheCysLeuHi sGlyGlyLeuSerF	: :		
Dd	1836	CTCTCTCATTTGGGAGAACTCTAGGACTTGTGATGATGCCACGATCTCAC	: :		
Qy	172	p-----ThrLeuAspHisIleArgAlaLeuAspArgIleGlnE	: :		
Dd	1896	CTCCTGTGAATAFACTTTAAACACCCCTGAGATATCCACACAGGGGTCAAG	: :		
Qy	187	oHisGluGlyProMetCysAspLeuLeu-----TrpSerAspProA	: :		
Dd	1956	CCACAGTGGGCCCAAGTCAGGAGCAGGTTGATTCAAATGGAAAACAGAAAGA	: :		
Qy	204	sGlyTrpGlyLysSerProArgGlyAlaGlyTyrThrPheGlyGlnAspI	: :		
Dd	2016	CTCTAAACGGGCGCTGATTCAGGCAATTTATCCAAGGAAGAGGGAAC	: :		
Qy	224	nPheAsnHisThrAsnGlyLeuSerLeuValAlaArg-----	: :		
Dd	2076	GATGTCAGCTTTAAACGAAGCCATGACTCAGATCAGGAGCTGGAGGAGA	: :		
Qy	237	----AlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAspLysA	: :		
Dd	2136	AGAGCTCAAGGAGATCATACAGCAAGGACCAGATCTGGCTTCAG-----	: :		

```
QY 255 rValpHeSerAlaProAsnTyr----- 262
Db 2187 GATGACCGAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGCGGAATCTGCTCT 2246
QY 263 -CysTyrArgCysGlyAsnMetAlaAlaileMetGluileAspGluThrMetAsnArgSe 282
Db 2247 GCGCCAGCAAGCCAGCAATTTCTGAGCCTGGAGATGTCATCAAGGCCTTACGCCTGGC 2306
QY 282 rPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLysThrPr 302
Db 2307 CATGCAGCTGGAAGAGCAGCGCTAGCAGACAAATAAGC-----AGCAAGAAACGGCC 2357
QY 302 p 302
Db 2358 C 2358

RESULT 14
US-10-955-054A-101
; Sequence 101, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 101
; LENGTH: 2740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-101

Alignment Scores:
Pred. No.: 18.7 Length: 2740
Score: 82.50 Matches: 68
Percent Similarity: 37.12% Conservative: 66
Best Local Similarity: 18.84% Mismatches: 156
Query Match: 4.94% Indels: 72
DB: 6 Gaps: 13

US-10-764-259-13 (1-306) x US-10-955-054A-101 (1-2740)
QY 4 TyrAlaAspValAspArgGlnIleGluGlnLeuSerGluCysLysPheProLeuSerGluLeu 23
Db 1174 TATGCCATGGCTCCCGGGACGCTCTTCCTCTGAA-GAATCAACCCCTGCTACCGGAAGTT 1232
QY 24 GluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGlu-TyrAsnValGl 43
Db 1233 GGGCGCTGAAGTCTATGTGACATTTTCGAGATCTACATGGAAGCTGTTGACCTGCT 1292
QY 43 nProValLysCysProValThrValCysGlyAsp-----IleHi 56
Db 1293 CAACAAGAAGCCAGCTCGCGTCTGGAGGACGGCAAGCAAGGTGCAAGTGGTGGG 1352
QY 56 sGlyGlnPheHis-----AspLeuIleGluLeuPheArgIleGlyGl 70
Db 1353 GCTCGAGGACATCTGGTTAACTCTGCTGATGATGTCATCAAGATGCTCGACATGGCGAG 1412
QY 70 yLysAlaProAspThrAsnTyrLeuPheMetGlyAspTyrValAspArgGlyTyrTyrSe 90
Db 1413 CGCCTGAGAACCTCGGCAGACATTTGCCAATCTCCATTCCTCCCGCTCCACGCGTG 1472
QY 90 rValGluThrValSerLeuLeuAlaLeuLysValArgTyrArgAspArgIleThrIl 110
Db 1473 CTTCCAA-----ATTATTCTTCGAGCTAAAGGGAGATGCATGGAAGTTCTCTTT 1523
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QY 110 e-----LeuArgGlyAsnHis----- 115
Db 1524 GGTAGATCTGCGAGGGAATGAGCGAGGCGGAGACACTTCCAGTGTGACAC 1583
QY 116 ---GluSerArgGlnIleThrGlnValTyrGlyPheTyrAspGluCysL 134
Db 1584 CATGAGGCGGCAGCAAGATCAACAAGAGTCTCTTAGCCCTCGAAGGAGTGCA 1643
QY 134 rGlyAsnAlaAsnValTrpLysTyrPheThrAsp-----LeuPheAspT 152
Db 1644 GGGCAGACAACAAGCTCACACCCCGTTCCGTGAGCAAGCAAGCTGCACAGG 1703
QY 152 uThrAlaLeuIleGluHisGluIlePheCysLeuHisGlyGlyLeuSerP 172
Db 1704 CTCCTTCATTTGGGGAACCTCTAGGACTTGATGATTCGCCACGATCTCAC 1763
QY 172 p-----ThrLeuAspHisIleArgAlaLeuAspArgIleGlnG 187
Db 1764 CTCCTGTGAATATACTTTAAACACCCTGAGATATGCAGACAGGGTCAAGG 1823
QY 187 oHisGluGlyProMetCysAspLeuLeu-----TrpSerAspProA 204
Db 1824 CCACAGTGGGCCAGTGGAGAGCAGTTGATTCAAAATGGAACACAGAGAGA 1883
QY 204 sGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspI 224
Db 1884 CTCTAACGGGGCGCTGATTCAGGCAATTTATCCAAAGNAGAGGAGGAAC 1943
QY 224 nPheAsnHisThrAsnGlyLeuSerLeuValAlaArg----- 236
Db 1944 GATGTCCAGCTTTAAACGAAGCCATGACTCAGATCAGGGAGCTGGAGGAGA 2003
QY 237 ---AlaHisGlnLeuValMetGluGlyTyrAsnTrpCysGlnAspLysA 255
Db 2004 AGAGCTCAAGGAGATCATACAGCAAGGACCAGACTGGCTTGAG----- 2054
QY 255 rValPheSerAlaProAsnTyr----- 262
Db 2055 GATGACCGAGCAGCCAGACTATGACCTGGAGACCTTTGTGAACAAAGCGG 2114
QY 263 -CysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrM 282
Db 2115 GGCCAGCAAGCAAGCATTTCTCAGCCCTCGAGATGTCATCAAGGCGCT 2174
QY 282 rPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrA 302
Db 2175 CATGCAGCTGGAAGAGCAGGCTAGCAGACAAATAAGC-----AGCA 2225
QY 302 p 302
Db 2226 C 2226

RESULT 15
US-11-121-086-13
; Sequence 13, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANAL
; FILE REFERENCE: 09138-6000-0000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 13
; LENGTH: 191797
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-13
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Alignment Scores:

Pred. No.:	1.19e+04	Length:	191797
Score:	82.50	Matches:	40
Percent Similarity:	35.80%	Conservative:	18
Best Local Similarity:	24.69%	Mismatches:	59
Query Match:	4.94%	Indels:	46
DB:	7	Gaps:	7

US-10-764-259-13 (1-306) x US-11-121-086-13 (1-191797)

Qy	126	PheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrpLysTyrPhe---Thr	144
Db	154760	TTTCTGGGTGACACCTTTAGGAGGTACCGGGATTAAACAAATATTTTACTTCCAGTT	154819
Qy	145	AspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIlePheCysLeuHis	164
Db	154820	CCCCACCTCTGCTATCACCTCTCACAACTTCATCCAGCATCAGCTTCTTTGC-----	154873
Qy	165	GlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAla-LeuAspArgIleG	184
Db	154874	-----CCTAAATTTAATCGTCATCTTATAAACTTGCTATTGCAAGAATTAT	154921
Qy	184	nGluValPro-----HisGluGlyPro-----	191
Db	154922	AAATATTCCTTTAACTGTGTAATGCTCTTTCAAACCATGGTCCCAAAATCCTCTACTA	154981
Qy	192	-----MetCysAspLeuLeuTipSerAspProAspAsp-----ArgCy	204
Db	154982	AAATTAAGCCTTCTTCCCAAGCATCTGGTGCCATAGCCATAGTCTTTTGAATG	155041
Qy	204	sGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAspIleAlaGluG	224
Db	155042	GGCTTGGGGAGATAATATATTACCAGGGCTTTACCATGGCTTTATCCATAGAGACTA	155101
Qy	224	nPheAsnHisThrAsnGlyLeuSerLeuValAlaAlaHisGlnLeuValMetGluG	244
Db	155102	GTTTAACAGAAGCTT-GGC-----CCGAGACATGG	155130
Qy	244	yTyrAsnTrp-----CysGlnAspLysAsnValThrValph	257
Db	155131	AGTGAATGGGACGCCAACAGGAGCAAGCTGTGTGAGGACAAATGTACACTCTCCATTTT	155190
Qy	257	eSer	258
Db	155191	CTCT	155194

Search completed: December 9, 2005, 13:18:29
Job time : 363 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 9, 2005, 09:50:51 ; Search time 163 Seconds

(without alignments)
1324.489 Million cell updates/sec

Title: US-10-764-259-13

Perfect score: 1670
Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPQSEPDVTRKTPDYFL 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1548	92.7	306	Q6VU05 LYCES	Q6VU05 lycopersico
2	1538	92.1	306	Q9MB06 VICFA	Q9MB06 vicia faba
3	1534	91.9	306	Q6VU06 LYCES	Q6VU06 lycopersico
4	1526	91.4	306	Q9FSV3 FAGSY	Q9FSV3 fagus sylv
5	1522	91.1	306	P2A1 ARATH	Q07998 arabidopsis
6	1519	91.0	306	Q9MB05 VICFA	Q9MB05 vicia faba
7	1514	90.7	306	Q8LAW8 ARATH	Q8LAW8 arabidopsis
8	1512	90.5	306	Q527K2 ORYSA	Q527K2 oryza sativ
9	1509	90.4	306	P2A3 HEVBR	Q9Z8E4 hevea brasl
10	1508.5	90.3	307	P2A3 ORYSA	Q9Z8E7 oryza sativ
11	1508.5	90.3	307	Q6Z6L9 ORYSA	Q6Z6L9 oryza sativ
12	1508	90.3	306	P2A2 ARATH	Q07999 arabidopsis
13	1506	90.2	306	P2A1 ORYSA	Q9Z8E3 oryza sativ
14	1501.5	89.9	305	P2A HELAN	P48579 helianthus
15	1495	89.5	307	P2A5 ARATH	Q04951 arabidopsis
16	1481	88.7	306	Q42981 ORYSA	Q42981 oryza sativ
17	1445	86.5	302	Q04859 TOBAC	Q04859 nicotiana t
18	1427	85.4	309	P2AA BOVIN	P67774 bos taurus
19	1427	85.4	309	P2AA HUMAN	P67775 homo sapien
20	1427	85.4	309	P2AA MOUSE	P63330 mus musculu
21	1427	85.4	309	P2AA PIG	P67776 sus scrofa
22	1427	85.4	309	P2AA RABIT	P67777 oryctolagus
23	1427	85.4	309	P2AA RAT	P63331 rattus norv
24	1427	85.4	309	Q58D70 BOVIN	Q58D70 bos taurus
25	1427	85.4	309	Q4RSN5 MACFA	Q4RSN5 m brain cdn
26	1426	85.4	309	Q5SNY5 MOUSE	Q5SNY5 mus musculu
27	1426	85.4	309	Q8WN16 CANFA	Q8WN16 canis faml1
28	1425	85.3	294	Q6Z6L8 ORYSA	Q6Z6L8 oryza sativ
29	1424	85.3	309	Q6P365 XENTR	Q6P365 xenopus tro
30	1424	85.3	309	Q5ZM47 CHICK	Q5ZM47 gallus gall
31	1421	85.1	309	Q8AVH9_XENTLA	Q8AVH9 xenopus lae

32	1419	85.0	309	Q619T8 HUMAN	Q619T8
33	1419	85.0	309	Q7ZVE7_BRARE	Q7ZVE7
34	1414.5	84.7	309	P2AA_CHICK	P4846
35	1413	84.6	309	Q5KGH3_CRYNE	Q5KGH3
36	1413	84.6	309	Q7PDD38_ANOGA	Q7PDD38
37	1412	84.6	309	P2A_PROME	P2365
38	1411	84.5	309	P2AB_HUMAN	P6271
39	1411	84.5	309	P2AB_MOUSE	P6271
40	1411	84.5	309	P2AB_RABIT	P1161
41	1411	84.5	309	P2AB_RAT	P6271
42	1411	84.5	309	Q8WZ56_HUMAN	Q8WZ56
43	1411	84.5	309	Q6P3K5_HUMAN	Q6P3K5
44	1411	84.5	309	Q803G3_BRARE	Q803G3
45	1410	84.4	309	Q6GLE6_XENTR	Q6GLE6

ALIGNMENTS

RESULT 1
Q6VU05 LYCES PRELIMINARY; PRT; 306 AA.

AC Q6VU05;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Protein phosphatase 2A catalytic subunit.
GN Name=PP2Ac2;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoty
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopers
OX NCBI_TaxId=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15125764; DOI=10.1111/j.1365-3113X.2004.02073.x;
RA He X., Anderson J.C., del Pozo O., Gu Y.-Q., Tang X., Marti
RT "Silencing of subfamily I of protein phosphatase 2A catalyt
RT results in activation of plant defense responses and local i
RT death.";
RL Plant J. 38:563-577(2004).
CC -I- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
CC phosphate.
CC -I- SIMILARITY: Belongs to the PPP phosphatase family.
CC EMBL; AY325818; AAQ67226.1; -; mRNA.
DR HSSP; 008209; 1AUI.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR004843; M:pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STEPHITASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA; 35009 MW; C0719F26F8FCA0E5 CRC64;

Query Match 92.7%; Score 1548; DB 2; Length 306
Best Local Similarity 91.2%; Pred. No. 4,2e-129;
Matches 279; Conservative 15; Mismatches 12; Indels

QY	1	MFSYADVDRQIEQLSECKPLSELEVKNCIDQARTTLVEEMVQPVKCPVT	QY	61	DIIEIFRIGKAPDNNYLFPMGDYVDGRGYYSVETVSLVALKVRVDRRTTI
DB	1	MFSHADLDRQIEQLMECKPLSEADYKTCIDQARALIVEEMVQPVKCPVT	QY	61	DIIEIFRIGKAPDNNYLFPMGDYVDGRGYYSVETVSLVALKVRVDRRTTI
DB	61	DIIEIFRIGKAPDNNYLFPMGDYVDGRGYYSVETVSLVALKVRVDRRTTI	QY	121	TQVYGFYDECLRKYGANAVWKYFTDLPDYLPPLALIEHIFCLHGLSPS
QY	121	TQVYGFYDECLRKYGANAVWKYFTDLPDYLPPLALIEHIFCLHGLSPS	QY	121	TQVYGFYDECLRKYGANAVWKYFTDLPDYLPPLALIEHIFCLHGLSPS
DB	121	TQVYGFYDECLRKYGANAVWKYFTDLPDYLPPLALIEHIFCLHGLSPS	QY	121	TQVYGFYDECLRKYGANAVWKYFTDLPDYLPPLALIEHIFCLHGLSPS

its

8 0;
FH 60
FY 60
OI 120
OI 120
AL 180
AL 180
AL 180

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QY 181 DRIOEVPHGPMCDLMSDPDRCGWISPRGAGTYFGODIAEQFNHTNGLSVARAHOL 240
DB 181 DRIOEVPHGPMCDLMSDPDRCGWISPRGAGTYFGODIASQFNHTNGLTISARAHOL 240
QY 241 VMEGINMCDKXNVVTFSAFNTCYRCGNMAAIMEIDETNRSFLQEPAPROSEPDPVTRK 300
DB 241 VMEGFNMCODKXNVVTFSAFNTCYRCGNMAAIMEIDETNRSFLQEPAPROSEPDPVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 2
Q9MB06_VICFA PRELIMINARY; PRT; 306 AA.
ID Q9MB06_VICFA PRELIMINARY; PRT; 306 AA.
AC Q9MB06;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type 2A protein phosphatase-1.
GN Name=vfpp2ac-1;
OS Vicia faba (Broad bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxID=3906;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ueno H., Kinoshita T., Aeanuma M., Shimazaki K.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AB039916; BAA92697.1; -; mRNA.
DR HSSP; P36873; 1176.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA; 34954 MW; 30C13CCDAB495DE7 CRC64;

Query Match 92.1%; Score 1538; DB 2; Length 306;
Best Local Similarity 90.8%; Pred. No. 3.3e-128;
Matches 278; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 MFSYADVDRIOEQLSECKPLSELEVKNLCDQARTILVEEMNVQPVKCPVTCGDHIGQFH 60
DB 1 MFSHADVDROIEQLMECKPLPEADVKALCDQARAILVEEMNVQPVKCPVTCGDHIGQFH 60
QY 61 DIIEIFRIGKAPDNTYLFMGDYVDRGYYSVETVSLVLAKVYRDRITTLRGNHRSROI 120
DB 61 DIIEIFRIGKAPDNTYLFMGDYVDRGYYSVETVSLVLAKVYRDRITTLRGNHRSROI 120
QY 121 TVYVGFYDECLRKRYGNANWKYFTDLFDYLPALTALIEHIEIFCHLHGLSPSLDTLDHIRAL 180
DB 121 TVYVGFYDECLRKRYGNANWKYFTDLFDYLPALTALIESQIFCHLHGLSPSLDTLDHIRAL 180
QY 181 DRIOEVPHGPMCDLMSDPDRCGWISPRGAGTYFGODIAEQFNHTNGLSVARAHOL 240
DB 181 DRIOEVPHGPMCDLMSDPDRCGWISPRGAGTYFGODIAEQFNHTNGLTISARAHOL 240
QY 241 VMEGINMCDKXNVVTFSAFNTCYRCGNMAAIMEIDETNRSFLQEPAPROSEPDPVTRK 300
DB 241 VMEGFNMCODKXNVVTFSAFNTCYRCGNMAAIMEIDETNRSFLQEPAPROSEPDPVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

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DB 301 TPDYFL 306

RESULT 3
Q6VU06_LYCES PRELIMINARY; PRT; 306 AA.
ID Q6VU06_LYCES PRELIMINARY; PRT; 306 AA.
AC Q6VU06;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein phosphatase 2A catalytic subunit.
GN Name=PP2Ac1;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopers
OX NCBI_TaxID=4081;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15125764; DOI=10.1111/j.1365-3113X.2004.02073.x;
RX He X., Anderson J.C., del Pozo O., Gu Y.-O., Tang X., Marti;
RT "Silencing of subfamily I of protein phosphatase 2A catalytic
RT results in activation of plant defense responses and local
RT death."
RL Plant J. 38:563-577(2004).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei;
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL; AY325817; AAQ67225.1; -; mRNA.
DR HSSP; O08209; 1AUI.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR004843; M-pesterase.
DR InterPro; IPR006186; T_phatase_apah.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PR00114; STPHPTASE.
DR ProDom; PD000252; T_phatase_apah; 1.
DR SMART; SM00156; PP2AC; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA; 35068 MW; 846BDSA03F63B107 CRC64;

Query Match 91.9%; Score 1534; DB 2; Length 306
Best Local Similarity 91.2%; Pred. No. 7.4e-128;
Matches 279; Conservative 12; Mismatches 15; Indels 3;

QY 1 MFSYADVDRIOEQLSECKPLSELEVKNLCDQARTILVEEMNVQPVKCPVT 27 60
DB 1 MFSHADVDROIEQLMECKPLSEAEVKTLCQARAILVEEMNVQPVKCPVT 27 60
QY 61 DIIEIFRIGKAPDNTYLFMGDYVDRGYYSVETVSLVLAKVYRDRITTLRGNHRSROI 120
DB 61 DIIEIFRIGKAPDNTYLFMGDYVDRGYYSVETVSLVLAKVYRDRITTLRGNHRSROI 120
QY 121 TVYVGFYDECLRKRYGNANWKYFTDLFDYLPALTALIEHIEIFCHLHGLSPSLDTLDHIRAL 180
DB 121 TVYVGFYDECLRKRYGNANWKYFTDLFDYLPALTALIESQIFCHLHGLSPSLDTLDHIRAL 180
QY 181 DRIOEVPHGPMCDLMSDPDRCGWISPRGAGTYFGODIAEQFNHTNGLSVARAHOL 240
DB 181 DRIOEVPHGPMCDLMSDPDRCGWISPRGAGTYFGODIAEQFNHTNGLTISARAHOL 240
QY 241 VMEGINMCDKXNVVTFSAFNTCYRCGNMAAIMEIDETNRSFLQEPAPROSEPDPVTRK 300
DB 241 VMEGFNMCODKXNVVTFSAFNTCYRCGNMAAIMEIDETNRSFLQEPAPROSEPDPVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 4
Q9FSV3_FAGSY PRELIMINARY; PRT; 306 AA.
ID Q9FSV3_FAGSY PRELIMINARY; PRT; 306 AA.

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AC 09FSV3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GN Protein phosphatase 2A.
Name=pp2a-1;
OS Fagus sylvatica (Beechnut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fagales; Fagaceae; Fagus.
NCBI_Taxid=28930;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=seed.
RA Gonzalez M., Nicolas C., Lorenzo O., Nicolas G., Rodriguez D.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
DR EMBL: AJ298829; CAC1129.1; -; mRNA.
DR HSP; P36873; 1UK7.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR004843; M-pesterase.
DR InterPro: IPR006186; T_phase_apah.
DR Pfam: PF00149; Metallophos. 1.
DR PRINTS: PR00114; STPHPHASE.
DR ProDom: PD000252; T_phase_apah; 1.
DR SMART: SM00156; PP2Ac; 1.
DR PROSITE: PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
KW Hydrolase; Iron.
SQ SEQUENCE 306 AA, 35023 MW; A0C0B40724F890EF CRC64;
Query Match 91.4%; Score 1526; DB 2; Length 306;
Best Local Similarity 89.5%; Pred. No. 3,8e-127;
Matches 274; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
Db 1 MSHYDVNRQITQLSECKRPLSELYKNUCDQARTIIIVEMNVPYKCPPTVCGDIIHGQFH 60
1 MSHSDILRQIEHLMCKRPLPEAEVKTLCDOARALIVEMNVPYKCPVTCGDIIHGFRY 60
61 DLIEFRIKQKAPDNTNLFMGDYVDGYSVETSLVLAIKRYVDRTIILGNHESROI 120
61 DLIEFRIKQKAPDNTNLFMGDYVDGYSVETSLVLAIKRYVDRTIILGNHESROI 120
61 DLIEFRIKQKAPDNTNLFMGDYVDGYSVETSLVLAIKRYVDRTIILGNHESROI 120
121 TQVGFYDECLARKYGNANVMKYFTDLFDYLPPLTALIEHEIFCLHGLSPSLDTLDIRAL 180
121 TQVGFYDECLARKYGNANVMKYFTDLFDYLPPLTALIEHEIFCLHGLSPSLDTLDIRAL 180
121 TQVGFYDECLARKYGNANVMKYFTDLFDYLPPLTALIEHEIFCLHGLSPSLDTLDIRAL 180
181 DRIOGVPHGPMCDLLMSPPDRCGWGISPRGAGYTFGQDIAEQRNHTNGLSLVARAOH 240
181 DRIOGVPHGPMCDLLMSPPDRCGWGISPRGAGYTFGQDIAEQRNHTNGLSLVARAOH 240
181 DRIOGVPHGPMCDLLMSPPDRCGWGISPRGAGYTFGQDIAEQRNHTNGLSLVARAOH 240
241 VMEGNYMCDKKNVVFSAFNVCYRCGNMAALIMEIDETNNRSFLQPEPAPOSEBDVTRK 300
241 VMEGNYMCDKKNVVFSAFNVCYRCGNMAALIMEIDETNNRSFLQPEPAPOSEBDVTRK 300
241 VMEGNYMCDKKNVVFSAFNVCYRCGNMAALIMEIDETNNRSFLQPEPAPOSEBDVTRK 300
Db 301 TPDYFL 306
301 TPDYFL 306
301 TPDYFL 306
RESULT 5
P2A1_ARATH STANDARD; PRT; 306 AA.
AC 007098;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-1 catalytic subunit
(EC 3.1.3.16).
OS Name=PP2A1; OrderedLocusNames=At1g10430; ORFNames=T10024.4;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabidopsi
NCBI_Taxid=3702;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Columbia GL1;
RX MEDLINE=93184204; PubMed=8382968;
RA Arino J., Perez-Callejon E., Cunillera N., Camps M., Posas
RA Ferrer A.;
RT "Protein phosphatases in higher plants: multiplicity of tyf
phosphatases in Arabidopsis thaliana.";
RL Plant Mol. Biol. 21:475-485(1993).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=1130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul
RA White O., Alonso J., Alafi H., Araujo R., Bowman C.L., Brc
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.K
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khayki
RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltz R., Marshall
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick
RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
RA Uteback T., Van Aken S., Vaysberg M., Vysotskaia V.S., We
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabid
thaliana.";
RL Nature 408:816-820(2000).
[3]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1086
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Souvick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Ch
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu C
RA Miranda M., Quach H.B., Tripp M., Chang C.H., Lee J.M., Tor
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K.,
RA Arakawa T., Banh Q., Banno F., Bowser L., Brooks S.Y., Carr
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hanse
RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Kai
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai
RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sa
RA Satou M., Tamae R., Vaysberg M., Wallender B.K., Wong C., Y
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.
RT "Empirical analysis of transcriptional activity in the Arab
genome.";
RL Science 302:842-846(2003).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
phosphate.
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similar
-1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2
subfamily.
CC
CC
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CC the European Bioinformatics Institute. There are no rest
CC use as long as its content is in no way modified and this e
CC removed.
CC
CC EMBL: M96733; AAA32848.1; -; mRNA.
CC
CC EMBL: AC007067; AAD39564.1; -; Genomic_DNA.
CC
CC EMBL: AY095847; AAL24329.1; -; mRNA.
CC
CC EMBL: AY093267; AAM13266.1; -; mRNA.
CC
CC PIR: S31162; S31162.

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DR InterPro; IPR004843; M-pestertase.  
DR InterPro; IPR006186; T.phrase_apah.  
DR Pfam; PF00149; Metallophos; 1.  
DR PRINTS; PR00114; STPHPHASE.  
DR ProDom; PD000252; T.phrase_apah; 1.  
DR SMART; SM00156; PP2Ac; 1.  
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.  
DR Hydrolyase; Iron; Manganese; Metal-binding; Multigene family;  
KM Protein phosphatase.  
FT ACT SITE 115 115 Proton donor (By similarity).  
FT METAL 54 54 Iron (By similarity).  
FT METAL 56 56 Iron (By similarity).  
FT METAL 82 82 Iron and manganese (By similarity).  
FT METAL 114 114 Manganese (By similarity).  
FT METAL 164 164 Manganese (By similarity).  
FT METAL 238 238 Manganese (By similarity).  
SQ SEQUENCE 306 AA; 34934 MW; B2DCB1B3C2CDD54F CRC64;  
  
Query Match 91.1%; Score 1522; DB 1; Length 306;  
Best Local Similarity 89.5%; Pred. No. 8 7e-127;  
Matches 274; Conservative 17; Mismatches 15; Indels 0; Gaps 0;  
  
QY 1 MESYADVDRQIEQLSECKPLSELEVNKLCDOARTILVEEMNVQPKVPCVTCGDHNGFH 60  
DB 1 MMSGDLDLROIQLMECKPLSEADVRLTCLDQARALIVEEYNQPKVPCVTCGDHNGFY 60  
  
QY 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITILGNHESROI 120  
DB 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITILGNHESROI 120  
  
QY 121 TVGVGFYDECLRKYGNAVMWKFTDLPDYLPPLTALIEHEIFCLHGLSPSLDTLDIRAL 180  
DB 121 TVGVGFYDECLRKYGNAVMWKFTDLPDYLPPLTALIEHQVFCFHGLSSSLDTLDIRSL 180  
  
QY 181 DRIQEVPHGPMCDLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTGLSIVARAHQL 240  
DB 181 DRIQEVPHGPMCDLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHNGLSISRAHQL 240  
  
QY 241 VMEGYNMCCDKXNVTVFSAPNYCYRCGNMAALMEIDETMNRSTLQEPAPRGSEPVYTK 300  
DB 241 VMEGYNMCCDKXNVTVFSAPNYCYRCGNMAALIEIGENNEQNLPDPAPROVEPDTTK 300  
  
QY 301 TPDYFL 306  
DB 301 TPDYFL 306  
  
Db 301 TPDYFL 306  
  
RESULT 6  
Q9MB05 VICEA PRELIMINARY; PRT; 306 AA.  
ID Q9MB05 VICEA PRELIMINARY; PRT; 306 AA.  
AC Q9MB05;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)  
DE Type 2A protein phosphatase-2.  
GN Name=vfpp2ac-2;  
OS Vicia faba (Broad bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.  
NCBI_TaxID=3906;  
RN [1]  
RX NUCLEOTIDE SEQUENCE.  
RA Ueno H., Kinoshita T., Asanuma M., Shimazaki K.;  
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
phosphate.  
CC -1- Similarity: Belongs to the PPP phosphatase family.  
DR EMBL; AA039917; BAA32698.1; -; mRNA.  
DR HSSP; P36873; 1UK7.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR004843; M-pestertase.
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DR InterPro; IPR006186; T.phrase_apah.  
DR Pfam; PF00149; Metallophos; 1.  
DR PRINTS; PR00114; STPHPHASE.  
DR ProDom; PD000252; T.phrase_apah; 1.  
DR SMART; SM00156; PP2Ac; 1.  
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.  
DR Hydrolyase; Iron.  
SQ SEQUENCE 306 AA; 35008 MW; F9DAB0D2EE72CC49 CRC64;  
  
Query Match 91.0%; Score 1519; DB 2; Length 306  
Best Local Similarity 89.9%; Pred. No. 1.6e-126;  
Matches 275; Conservative 16; Mismatches 15; Indels 0;  
  
QY 1 MESYADVDRQIEQLSECKPLSELEVNKLCDOARTILVEEMNVQPKVPCVTC 60  
DB 1 MMSGDLDLROIQLMECKPLSEADVRLTCLDQARALIVEEYNQPKVPCVTC 60  
  
QY 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITIL 120  
DB 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITIL 120  
  
QY 121 TVGVGFYDECLRKYGNAVMWKFTDLPDYLPPLTALIEHEIFCLHGLSPS 180  
DB 121 TVGVGFYDECLRKYGNAVMWKFTDLPDYLPPLTALIEHQVFCFHGLSPS 180  
  
QY 181 DRIQEVPHGPMCDLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTNG 240  
DB 181 DRIQEVPHGPMCDLMSDDPDDRCMGISPRGAGYTFGQDIAEQFNHTNG 240  
  
QY 241 VMEGYNMCCDKXNVTVFSAPNYCYRCGNMAALMEIDETMNRSTLQEPAP 300  
DB 241 VMEGYNMCCDKXNVTVFSAPNYCYRCGNMAALIEIGENNDQNFLOFDPAP 300  
  
QY 301 TPDYFL 306  
DB 301 TPDYFL 306  
  
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RESULT 7  
Q8LAW8 ARATH PRELIMINARY; PRT; 306 AA.  
ID Q8LAW8 ARATH PRELIMINARY; PRT; 306 AA.  
AC Q8LAW8;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, last annotation update)  
DE Serine/threonine protein phosphatase type 2a, putative.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids  
NCBI_TaxID=3702;  
RN [1]  
RX NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22088475; PubMed=12093376;  
RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov  
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;  
RT "Full-length messenger RNA sequences greatly improve genome  
annotation."  
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).  
RN [2]  
RX NUCLEOTIDE SEQUENCE.  
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.  
RA Feldmann K.;  
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +  
phosphate.  
CC -1- Similarity: Belongs to the PPP phosphatase family.  
DR EMBL; AY087557; AAM65099.1; -; mRNA.  
DR HSSP; P36873; 1IT6.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR InterPro; IPR004843; M-pestertase.  
DR InterPro; IPR006186; T.phrase_apah.  
DR Pfam; PF00149; Metallophos; 1.
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DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydrolase; Iron; Manganese; Metal-binding; Multigene family;
KM Protein phosphatase.
FT ACT_SITE 115 115 Proton donor (By similarity).
FT METAL 54 54 Iron (By similarity).
FT METAL 56 56 Iron (By similarity).
FT METAL 82 82 Iron and manganese (By similarity).
FT METAL 114 114 Manganese (By similarity).
FT METAL 154 154 Manganese (By similarity).
FT METAL 238 238 Manganese (By similarity).
SQ SEQUENCE 306 AA; 34969 MW; EFBE7FDFAEBA61 CRC64;

Query Match
Best Local Similarity 90.4%; Score 1509; DB 1; Length 306;
Matches 273; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MVSADVDRQIQEQLSECKPLSELEVNKLCDAQRTILVEENWQPVKCPVTGCDIHGQF 60
DB 1 MSHSGDLDRQIAQLRECHLAEGEVRALCEQAKILMEENWQPVRCV
QY 61 DLIELFRIIGKAPDNTNLYFMGDIYDRGYYSVETVSLVALKVRDRRTITLRGNHESRQI 120
DB 61 DLIELFRIIGKAPDNTNLYFMGDIYDRGYYSVETVSLVALKVRDRRTITLRGNHESRQI 120
QY 121 TQVYGFYDECLRRKGNANWVKYFTDLFDYLPPLTALIEHEIFCLAGLSPLDTLDIRAL 180
DB 121 TQVYGFYDECLRRKGNANWVKYFTDLFDYLPPLTALIEHQIFCLHGLSLSDTLDIRAL 180
QY 181 DRIQEVPHBGMCDLWSPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSIVARHQL 240
DB 181 DRIQEVPHBGMCDLWSPDDRCGWSISPRGAGYTFGQDIAEQFNHTNGLSIVARHQL 240
QY 241 VMEGYNMCDKNVTVTSAPNYCYRCGMAALMEIDETMRSLOEAPRQSEPRVTXK 300
DB 241 VMEGYNMCDKNVTVTSAPNYCYRCGMAALIEIGENMAQNFLODPAPRQIPEPTTK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 10
P2A3 ORYSA STANDARD; PRT; 307 AA.
ID P2A3 ORYSA 09XGT7;
AC 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-3 catalytic subunit
DE (EC 3.1.3.16).
GN Name=PP2A3;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Indica / IR36;
RA Yu R.M.K., Kong R.Y.C.;
RT Molecular cloning and characterization of protein phosphatase 2A
RT catalytic subunit genes from Oryza sativa."
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2A
CC subfamily.
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CC use as long as its content is in no way modified and this s
CC removed.
CC -----
CC EMBL; AF159061; AAD41126.1; -; Genomic_DNA.
CC HSSP; P08129; 1PTM.
CC Gramene; O9XGT7; -.
CC InterPro; IPR004843; M-esterase.
CC InterPro; IPR006186; T_phase_apah.
CC Pfam; PF00149; Metallophos; 1.
CC PRINTS; PR00114; STEPHATAS.
CC PRODOM; PD000252; T_phase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydrolase; Iron; Manganese; Metal-binding; Multigene family
KM Protein phosphatase.
FT ACT_SITE 116 116 Proton donor (By similarity).
FT METAL 55 55 Iron (By similarity).
FT METAL 57 57 Iron (By similarity).
FT METAL 83 83 Iron and manganese (By similar
FT METAL 115 115 Manganese (By similarity).
FT METAL 165 165 Manganese (By similarity).
FT METAL 239 239 Manganese (By similarity).
SQ SEQUENCE 307 AA; 35145 MW; 97143563695D0DD6 CRC64;

Query Match
Best Local Similarity 88.6%; Score 1508.5; DB 1; Length 3.
Matches 272; Conservative 23; Mismatches 11; Indels

QY 1 MVSADVDRQIQEQLSECKPLSELEVNKLCDAQRTILVEENWQPVKCPV
DB 1 MSHSGDLDRQIAQLRECHLAEGEVRALCEQAKILMEENWQPVRCV
QY 60 HDLIELFRIIGKAPDNTNLYFMGDIYDRGYYSVETVSLVALKVRDRRTIT
DB 61 DLIELFRIIGKAPDNTNLYFMGDIYDRGYYSVETVSLVALKVRDRRTIT
QY 120 ITQVYGFYDECLRRKGNANWVKYFTDLFDYLPPLTALIEHEIFCLAGLSP
DB 121 ITQVYGFYDECLRRKGNANWVKYFTDLFDYLPPLTALIEHQVCLHGLSP
QY 180 IDRIQEVPHBGMCDLWSPDDRCGWSISPRGAGYTFGQDIAEQFNHTN
DB 181 IDRIQEVPHBGMCDLWSPDDRCGWSISPRGAGYTFGQDIAEQFNHTN
QY 240 LYMEGYNMCDKNVTVTSAPNYCYRCGMAALMEIDETMRSFLOEAPR
DB 241 LYMEGYNMCDKNVTVTSAPNYCYRCGMAALIEIGENMDQNFLODP
QY 300 KTPDYFL 306
DB 301 KTPDYFL 307

RESULT 11
Q6Z6L9 ORYSA PRELIMINARY; PRT; 307 AA.
ID Q6Z6L9;
AC 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-3 catalytic subun
GN Name=P0027A02.2-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
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CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -1- SIMILARITY: Belongs to the PPP phosphatase family.
 CC EMBL: AP004996; EMBL174.1; -; Genomic_DNA.
 CC DR HSSP: Q08209; 1AU1.
 CC DR Gramene; Q62619; -;
 CC DR GO: GO:0016787; P:hydrolyase activity; IEA.
 CC DR InterPro: IPR004843; M-esterase.
 CC DR InterPro: IPR006186; T_phatase_apah.
 CC DR Pfam: PF00149; Metallophos; 1.
 CC DR PRINTS: PR00114; STPHPHASE.
 CC DR ProDom: PD000252; T_phatase_apah; 1.
 CC DR SMART: SM00156; PP2Ac; 1.
 CC DR PROSITE: PS00125; SER_THR_PHOSPHATASE; UNKNOWN_1.
 CC DR Hydrolyase; Iron.
 CC SEQ SEQUENCE 307 AA; 35144 MW; 97143563695D0DD6 CRC64;
 Query Match 90.3%; Score 1508.5; DB 2; Length 307;
 Best Local Similarity 88.6%; Pred. No. 1.4e-125;
 Matches 272; Conservative 23; Mismatches 11; Indels 1; Gaps 1;

QY 1 MD SYADVDRQIEQISECKPISELEVKMLCDQARTILVEEMNVQPKCPVTGDIHQGF 59
 DB 1 WESSHGDLDROIAQLRECGHLAGGEVRAICQAKAILMEEMVQPRCPVTGDIHQGF 60
 QY 60 HLLIELFRIGGAPDNTNIFMGDYDRGYSVETVSLVALKVRTRDRTILRGNHESQ 119
 DB 61 YLIELFRIGGAPDNTNIFMGDYDRGYSVETVSLVALKVRTRDRTILRGNHESQ 120
 QY 120 IYQVGFVDEGCRKGNANVMKFTDLPYLLPTLALIEHIFCLGSGSPSLDTLDHRA 179
 DB 121 ITQVGFVDEGCRKGNANVMKFTDLPYLLPTLALIEHIFCLGSGSPSLDTLDHRA 180
 QY 180 LDRIGVEPHGPMCDLMSDPDRCGWGISPRAGYTFGCDIAEOPFNHTGSLVARAQ 239
 DB 181 LDRIGVEPHGPMCDLMSDPDRCGWGISPRAGYTFGCDIAEOPFNHTGSLVARAQ 240
 QY 240 LVMGYNVQODKQNVTVTFSAFNYCYRCGNMAIMEIDFNMSFLQEPAPQSEBDVTR 299
 DB 241 LVMGYNVQODKQNVTVTFSAFNYCYRCGNMAIMEIDFNMSFLQEPAPQSEBDVTR 300
 QY 300 KTPDYFL 306
 DB 301 KTPDYFL 307

RESULT 12
 P2A2 ARATH STANDARD; PRT; 306 AA.
 AC 007099;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Serine/threonine protein phosphatase PP2A-2 catalytic subunit (EC 3.1.3.16).
 OS Name=PP2A2; OrderedLocustNames=At1g59830; ORENames=F23H11.15;
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; OC rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX NUCLEOTIDE SEQUENCE.
 RC STRAIN=cv. Columbia G11;
 RX MEDLINE=93184204; PubMed=8382968;
 RA Arino J., Perez-Callejon E., Cunillera N., Camps M., Posas F., Ferrer A.,
 RT "Protein phosphatases in higher plants: multiplicity of type 2A phosphatases in Arabidopsis thaliana.";
 RL Plant Mol. Biol. 21:475-485(1993).
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;

RX MEDLINE=21016719; PubMed=1130712; DOI=10.1038/35048500;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul White O., Alonso J., Altarfi H., Araujo R., Bowman C.L., Brice B., Buerkle E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.K., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khayki Kim C.T., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltl R., Marzall Miltseher J., Miranda M., Nguyen M., Nierman W.C., Osborne Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southcote Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utecherback T., Van Aken S., Vayberg M., Vysotskaia V.S., Wu W.D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana";
 RL Nature 408:816-820(2000).
 RN (3)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1086 Yamada K., Lam J., Dale J.M., Chen H., Shinn P., Palm C.J., Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Ch Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G Mirinda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tor Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carr Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hanse Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Kai Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sa Saito M., Tame R., Vayberg M., Wallender E.K., Wong C., Y Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.
 RT "Empirical analysis of transcriptional activity in the Arab genome.";
 RL Science 302:842-846(2003).
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -1- COPACITOR: Binds 1 iron ion per subunit (By similarity).
 CC -1- COPACITOR: Binds 1 manganese ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the PPP phosphatase family. PP-2 subfamily.
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 CC -----
 CC EMBL: M96732; AAA32847.1; -; mRNA.
 CC EMBL: AC007258; AAD39326.1; -; Genomic_DNA.
 CC EMBL: AY063942; AAL36298.1; -; mRNA.
 CC EMBL: AY06543; AAM20193.1; -; mRNA.
 CC DR PIR: S31161; S31161.
 CC DR HSSP: P36873; 1176.
 CC DR InterPro: IPR004843; M-esterase.
 CC DR InterPro: IPR006186; T_phatase_apah.
 CC DR Pfam: PF00149; Metallophos; 1.
 CC DR PRINTS: PR00114; STPHPHASE.
 CC DR ProDom: PD000252; T_phatase_apah; 1.
 CC DR SMART: SM00156; PP2Ac; 1.
 CC DR PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
 CC DR Hydrolyase; Iron; Manganese; Metal-binding; Multigene family
 CC Protein phosphatase.
 CC ACT SITE 115
 CC FT METAL 54
 CC FT METAL 54
 CC FT METAL 56
 CC FT METAL 82
 CC FT METAL 114
 CC FT METAL 114
 CC Proton donor (By similarity).
 CC Iron (By similarity).
 CC Iron and manganese (By similarity).
 CC Manganese (By similarity).

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FT METAL 164 164 Manganese (By similarity).
FT METAL 238 238 Manganese (By similarity).
SQ SEQUENCE 306 AA, 34961 MW, 579427029D41A1C1 CRC64;

Query Match
Best Local Similarity 88.9%; Score 1508; DB 1; Length 306;
Matches 272; Conservative 17; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSHYADVROROIQLSECKRPLSELYKNCIDQARTILVEBNVQPKCPYTVGGDIHGQPH 60
DB 1 MFLNGDLRQIQLEQMECKRPLGEADVKKILCDQAKALIVEBNVQPKCPYTVGGDIHGQY 60
QY 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRRTITLGNHESROI 120
DB 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRRTITLGNHESROI 120
QY 121 TVGVGFYDECKLRKYGANVAMWKYFTDLFDYLPPLTALIEHIEIFCLHGLSPSLDTHIRAL 180
DB 121 TVGVGFYDECKLRKYGANVAMWKYFTDLFDYLPPLTALIEHIEIFCLHGLSPSLDTHIRSL 180
QY 181 DRIOGVPHRGPCDILMSDPDRCGWGISPRGAGYTFGQDIAEOFNHTNGLSIVARHQL 240
DB 181 DRIOGVPHRGPCDILMSDPDRCGWGISPRGAGYTFGQDIAEOFNHTNGLSIVARHQL 240
QY 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOEPAPROSEPDVTRK 300
DB 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOEPAPROSEPDVTRK 300
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 13
P2A1_ORYSA STANDARD; PRT; 306 AA.
AC Q92SS3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine protein phosphatase PP2A-1 catalytic subunit
DE (EC 3.1.3.16).
GN Name=PP2A1;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Indica / IR36;
RA Yu R.M.K., Zhou Y., Xu P., Kong R.Y.C.;
RT "Isolation and characterization of a rice gene encoding a catalytic
RT subunit of protein phosphatase 2A."
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -|- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: Belongs to the PPP phosphatase family. PP-2A
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AF097182; AAC72838.1; -; Genomic_DNA.
CC HSSP, P08129; IFDM.
CC Gramene; Q92SS3; -.
CC InterPro; IPR004843; M-esterase.

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DR InterPro; IPR006186; T_phase_apah.
DR Pfam; PF00149; Metallophos. 1.
DR PRINTS; PR00114; STRPHTRASE.
DR ProDom; PD000252; T_phase_apah; 1.
DR SMART; SM00156; PP2Ac; 1.
DR PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
KW Hydroxylase; Iron; Manganese; Metal-binding; Multigene family
KW Protein phosphatase.
FT ACT_SITE 115 115 Proton donor (By similarity).
FT METAL 54 54 Iron (By similarity).
FT METAL 56 56 Iron (By similarity).
FT METAL 82 82 Iron and manganese (By similar
FT METAL 114 114 Manganese (By similarity).
FT METAL 164 164 Manganese (By similarity).
FT METAL 238 238 Manganese (By similarity).
SQ SEQUENCE 306 AA; 35128 MW; 5DC7F99510E272F9 CRC64;

Query Match
Best Local Similarity 87.6%; Score 1506; DB 1; Length 306
Matches 268; Conservative 25; Mismatches 13; Indels 0;

QY 1 MSHYADVROROIQLSECKRPLSELYKNCIDQARTILVEBNVQPKCPYT
DB 1 MSHADLDRQISQLRECKRPLGEAEVRALCEQAKALIMERNVQPKCPYT
QY 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITTI
DB 61 DLIELFRIGKAPDNTNLYFMGDIYVDRGYYSVETVSLVALKRYRDRITTI
QY 121 TVGVGFYDECKLRKYGANVAMWKYFTDLFDYLPPLTALIEHIEIFCLHGLSPS;
DB 121 TVGVGFYDECKLRKYGANVAMWKYFTDLFDYLPPLTALIEHIEIFCLHGLSPS;
QY 181 DRIOGVPHRGPCDILMSDPDRCGWGISPRGAGYTFGQDIAEOFNHTNG;
DB 181 DRIOGVPHRGPCDILMSDPDRCGWGISPRGAGYTFGQDIAEOFNHTNG;
QY 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOEPAPV
DB 241 VMEGYNMCCDKKVVTVFSAPNYCYRCGNMAAIMEIDETNRSFLOEPAPV
QY 301 TPDYFL 306
DB 301 TPDYFL 306

RESULT 14
P2A1_HELAN STANDARD; PRT; 305 AA.
AC P48579;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine protein phosphatase PP2A catalytic subunit
DE (EC 3.1.3.16).
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicot;
OC Asterids; Campanulids; Asterales; Asteraceae; Asteroidae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Root meristem;
RA MEDLINE=9539397; PubMed=7664759;
RA Menzel D., Vuorek O., Frank S., Eisner-Menzel C.;
RT "Protein phosphatase 2A, a potential regulator of actin dyn
RT actin-based organelle motility in the green alga Acetabular
RL Eur. J. Cell Biol. 67:179-187(1995).
CC -|- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
CC phosphate.
CC -|- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -|- COFACTOR: Binds 1 manganese ion per subunit (By similar

```

CC -1- SIMILARITY: Belongs to the PPP phosphatase family. pp-2A
CC subfamily.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: Z26041; CAA81126.1; -, mRNA.
CC PIR: S37086; S37086.
CC HSSP: P08129; 1FMW.
CC InterPro: IPR004843; M-esterase.
CC InterPro: IPR006186; T_phatase_apah.
CC Pfam: PF00149; Metallophos; 1.
CC PRINTS: PR00114; STRPHATSE.
CC PRODOM: PD000252; T_phatase_apah; 1.
CC SMART: SM00156; PP2Ac; 1.
CC PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
CC Hydroxylase; Iron; Manganese; Metal-binding; Multigene family;
CC Protein phosphatase.
CC ACT SITE 114 114 Proton donor (By similarity).
FT METAL 53 53 Iron (By similarity).
FT METAL 55 55 Iron (By similarity).
FT METAL 81 81 Iron and manganese (By similarity).
FT METAL 113 113 Manganese (By similarity).
FT METAL 163 163 Manganese (By similarity).
FT METAL 237 237 Manganese (By similarity).
SQ SEQUENCE 305 AA; 34865 MW; 0B9D14F3DD0E950 CRC64;

Query Match 89.9%; Score 1501.5; DB 1; Length 305;
Best Local Similarity 88.2%; Pred. No. 5,8e-125;
Matches 270; Conservative 21; Mismatches 14; Indels 1; Gaps 1;

QY 1 MSYADVDRQIQSLSECKPLSELEVNKLCDOARTILVEEMNQPVKCPVTCGDHGGH 60
DB 1 MSQSGLDLDQIHLMDCKLPE-EVRTLCDQARTILVEEMNQPVKCPVTCGDHGGH 59

QY 61 DLIELFRIGKAPDTNYLFMGDYVDRGYVETSLVLAALKVRYDRITILGNHESROI 120
DB 60 DLIELFRIGSAPDTNYLFMGDYVDRGYVETSLVLAALKVRYDRITILGNHESROI 119

QY 121 TQVGFYDECLAKKYGNAWVKFTDLFDYLPFTALIEHIFCLHGLSGLDTHIRAL 180
DB 120 TQVGFYDECLAKKYGNAWVKFTDLFDYLPFTALIEHIFCLHGLSGLDTHIRAL 179

QY 181 DRIOEVPEHGPICDLSPDDRCGMSIPRGAGYFEGODIABOPHTNGLSIVARHQL 240
DB 180 DRIOEVPEHGPICDLSPDDRCGMSIPRGAGYFEGODIABOPHTNGLSIVARHQL 239

QY 241 VMEGYNMCDKXNVTVFSAPNYCYRCGNAALMEIDETNRSFLQEPAPROSEPDVTER 300
DB 240 VMEGYNMCDKXNVTVFSAPNYCYRCGNAALMEIDETNRSFLQEPAPROSEPDVTER 299

QY 301 TPDYFL 306
DB 300 TPDYFL 305

OK NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=cv. Columbia;
RA Stamey R.T., Rundle S.J.;
RT "Characterization of a novel isoform of a type 2A serine/th
RT protein phosphatase from Arabidopsis thaliana.";
RL (ex) Plant Gene Register PCR95-116.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.U., Federspiel N.L., Kaul
RA White O., Alonso J., Altabi H., Araujo R., Bowman C.L., Brc
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressey T.H.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Feng B., Fuji
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khayki
RA Kim C.U., Koo H.L., Kremetska I., Kurtz D.B., Kwan A.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani
RA Miltoscher J., Miranda M., Nguyen M., Nierman W.C., Osborne
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwic
RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,
RA Utecherback T., Van Aken S., Vayberg M., Vysotskaia V.S., Wa
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabid
RT thaliana.";
RL Nature 408:816-820(2000).
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protei
CC phosphate.
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similar
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the PPP phosphatase family. pp-2
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through
CC between the Swiss Institute of Bioinformatics and the EMB
CC the European Bioinformatics Institute. There are no restr
CC use as long as its content is in no way modified and this s
CC removed.
CC -----
CC EMBL: U39568; AAC668.1; -, mRNA.
CC EMBL: AC002062; AAB611.6.1; -, Genomic DNA.
CC EMBL: AC010675; AAG52565.1; -, Genomic DNA.
CC PIR: B96722; B96722.
CC HSSP: P36873; 1IT6.
CC InterPro: IPR004843; M-esterase.
CC InterPro: IPR006186; T_phatase_apah.
CC Pfam: PF00149; Metallophos; 1.
CC PRINTS: PR00114; STRPHATSE.
CC PRODOM: PD000252; T_phatase_apah; 1.
CC SMART: SM00156; PP2Ac; 1.
CC PROSITE: PS00125; SER_THR_PHOSPHATASE; 1.
CC Hydroxylase; Iron; Manganese; Metal-binding; Multigene family;
CC Protein phosphatase.
CC ACT SITE 116 116 Proton donor (By similarity).
FT METAL 55 55 Iron (By similarity).
FT METAL 57 57 Iron (By similarity).
FT METAL 83 83 Iron and manganese (By similar
FT METAL 115 115 Manganese (By similarity).
FT METAL 165 165 Manganese (By similarity).
FT METAL 239 239 Manganese (By similarity).
SQ SEQUENCE 307 AA; 35042 MW; D00149EAD0E20C82F CRC64;

Query Match 89.5%; Score 1495; DB 1; Length 307
Best Local Similarity 87.9%; Pred. No. 2.2e-124;
Matches 268; Conservative 23; Mismatches 14; Indels

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Db	3	PATGDI DRQIEQUMECKALSETEVKMLCEHAKTILVEEYNQPVKCPVTVCGBD IHGQFYD	62
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Db	63	LIELFRIGSSPPTNYLFMGDYVDRCGYSEVETVSLVALKVRDRITILRGNHESROIT	122
Qy	122	QYGFYDECTLRKXGNANVMKYFTDLFDYLPLFTALIEHEIFCLHGLSPSLDTLDHIRALD	181
Db	123	QYGFYDECTLRKXGNANVMKYFTDLFDYLPLFTALIESQVFC LHGLSPSLDTLDHIRSLD	182
Qy	182	RIQEVPHESGPMCDLMSDPDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHOLV	241
Db	183	RIQEVPHESGPMCDLMSDPDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHOLV	242
Qy	242	MEGYNNCQDKNVTYVTSAPNYCYRCGNMAIMEIDETNRSFLQEPAPROSEPDVTRKT	301
Db	243	MEGYNNCQDKNVTYVTSAPNYCYRCGNMAIMEIDETNRSFLQEPAPROSEPDVTRKT	302
Qy	302	PDYFL 306	
Db	303	PDYFL 307	

Search completed: December 9, 2005, 10:23:18
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 9, 2005, 10:24:12 ; Search time 4445 Seconds
(without alignments)
3913.182 Million cell updates/sec

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Perfect score: 1670
Sequence: 1 MFSYADVDRQIEQLSECKPL.....EPAPRQSPDVTRKTPDYFL 306

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US10764259/runat_05122005_094547_7015/app_query.fasta_1.455
-DB=GenEmbl -QMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blowm62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10764259 @CGN 1.1 7415 @runat_05122005_094547_7015 -NCFU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.in.*
- 3: gb.env.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.sts.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.htg.*
- 15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1670	100.0	1365	6	AX490719 Sequence
3	1548	92.7	1511	15	AY325818 Lycopersi

ALIGNMENTS

RESULT 1	AR606281	Sequence 8 from patent US 6818805.	1365 bp	DNA	linear	EC-2004
LOCUS	AR606281					
DEFINITION	AR606281					
ACCESSION	AR606281					
VERSION	AR606281.1	GI:56658183				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1365)					
AUTHORS	da Costa e Silva,O., Bohnert,H.J., van Thielen,N., C					
	ishitani,M.					
TITLE	Phosphatase stress-related proteins and methods of u					
JOURNAL	Patent: US 6818805-A 8 16-NOV-2004;					
	BASF Plant Science GmbH; Ludwigshafen;					
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	/mol_type="genomic DNA"					
ORIGIN						
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Score:	1670.00					Matches: 306
Percent Similarity:	100.00%					Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-764-259-13 (1-306) x AR606281 (1-1365)

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DB 131 TCGGAGTTGGAGTGNAGAACCTATGTGATCAAGCTCGACCATCTTGTGTGGAGGATGG 190
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
DB 191 AACGTGCAGCCGTAAGTGTCTGTACGGTTTCGGGTGACATCCATGCCAGTTTCAT 250
QY 61 AspLeuIleGluLeuPheArgIleGlyIysAlaProAspThrAsnTyrIleuPheMet 80
DB 251 GATCTCATCGAGCTTTTCGCGATAGGAGCAAGCGGCCGACACCAACTACTTGTTCATG 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100
DB 311 GCGGACTATGTGGATCGTGATATATCTCTCGAGACTGTGTCTCTTATGTGACCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSerArgGlnIle 120
DB 371 AAGTGGCGGTATAGGATAGGATCAATCTTTCGGAGGGAACCCAGAGAGCGAGATT 430
QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAlaAsnValTrp 140
DB 431 ACGCAAGTATATGGTTTCTATGATGAATCCCTCGCGAAGTATGGAATCGAATGTTGG 490
QY 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGluHisGluIle 160
DB 491 AAGTACTTCACGATCTGTTTCGACTACCTGCTCTGACAGCTCTCATTTGAGCACGAGAT 550
QY 161 PheCysLeuHisGlyIleGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
DB 551 TTTTGTCTTCATGGTGTCTGTCTCCATCGCTCGACACATTAGATCACATCCGAGCCCTA 610
QY 181 AspArgIleGlnValProHisGluGlyProMetCysAspLeuLeuTrpSerAspPro 200
DB 611 GATCGTATTTCAAGAGTGGCGCACGAGGCCCGGATGTGTGATCTACTCTGTCTGATCCA 670
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DB 671 GATGATCGTTTGGATGGGGCAATTTCCACGAGGTGCCGGTTATATCTTTTGGTCAAGAT 730
QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
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DB 791 GTGATGGAAGGATACAAATTTGGTGCCAGGATAAAATGTTGTACAGTTTTCAGTCCCCC 850
QY 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
DB 851 AATTACTGTACCGCTGTGGACATGGCGCCCATATATGGATAGATGATGATGATGAT 910
QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
DB 911 CGGTCTTTTCTTCAGTTTCGAAACGAGCACCGCGCAAGTGAACCATGTGTGACGCGGAAG 970
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RESULT 2
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LOCUS

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ACCESSION AX490719
VERSION AX490719.1 GI:22323691
KEYWORDS
SOURCE Physcomitrella patens
ORGANISM Physcomitrella patens
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
AUTHORS Bryopsida; Funariidae; Funariales; Funariaceae; Phys-
da Costa,E.S., Bohnert,H.J., Ishitani,M., van Thielel
Chan,R.
Phosphatase stress-related proteins and methods of u
Patent: WO 0246442-A 8 13-JUN-2002;
BASf Plant Science GmbH (DE)
FEATURES
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/organism="Physcomitrella patens"
/mol_type="unassigned DNA"
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Score: 1670.00 Matches: 306
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-764-259-13 (1-306) x AX490719 (1-1365)
QY 1 MetProSerTyrAlaAspValAspArgGlnIleGluInLeuSerGluCys 20
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QY 21 SerGluLeuGluValIysAsnLeuCysAspGlnAlaAtrGThrIleLeuVal 40
DB 131 TCGGAGTTGGAGTGAAGAACCTATGTGATCAAGCTCGAGCTCGACCATCTTGGT 190
QY 41 AsnValGlnProValIysCysProValThrValCysGlyAspIleHisGly 60
DB 191 AACGTGCAGCCGTAAGTGTCTGTACGGTTTCGGGTGACATCCATGCCAGTGG 250
QY 61 AspLeuIleGluLeuPheArgIleGlyIysAlaProAspThrAsnTyr 80
DB 251 GATCTCATCGAGCTTTTCGCGATAGGAGCAAGCGGCCGACACCAACTACTTGTTCAT 310
QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu 100
DB 311 GCGGACTATGTGGATCGTGATATATCTCTCGAGACTGTGTCTCTTATGTGACCCCTG 370
QY 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSer 120
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QY 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAla 140
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DB 491 AAGTACTTCACGATCTGTTTCGACTACCTGCTCTGACAGCTCTCATTTGAGCACGAGAT 550
QY 161 PheCysLeuHisGlyIleGlyLeuSerProSerLeuAspThrLeuAspHis 180
DB 551 TTTTGTCTTCATGGTGTCTGTCTCCATCGCTCGACACATTAGATCACATCCGAGCCCTA 610
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QY 241 ValMetGluGlyTyrAsnTrpCysGlnAspIysAsnValValThrValPhe 260
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QY 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspVal 300
DB 911 CGGTCTTTTCTTCAGTTTCGAAACGAGCACCGCGCAAGTGAACCATGTGTGACGCGGAAG 970
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DB 971 ACTCCTGATTACTTTCTG 988
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Db 671 GATGATCGTTGTGGATGGGCAATTCACCACGAGTGGCGGTTATACCTTTTGGTCAAGAT 730
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Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 911 CGGTCTTTCTTCAGTTCGAACCAAGCCGCGGCAAGTGAACCAAGATGTGACGCGGAAG 970
Qy 301 ThrProAspTyrPheLeu 306
Db 971 ACTCCTGATTACTTCTG 988

RESULT 3
AY325818 1511 bp mRNA linear PLN 05-MAY-2004
LOCUS Lycopersicon esculentum protein phosphatase 2A catalytic subunit
DEFINITION (PP2Ac2) mRNA, complete cds.
ACCESSION AY325818
VERSION AY325818.1 GI:34398262
KEYWORDS Lycopersicon esculentum (Solanum lycopersicum)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 1511)
He,X., Anderson,J.C., Pozo Od.O., Gu,Y.Q., Tang,X. and Martin,G.B.
Silencing of subfamily I of protein phosphatase 2A catalytic
subunits results in activation of plant defense responses and
localized cell death
Plant J. 38 (4), 563-577 (2004)
15125764
JOURNAL PUBMED
REFERENCE 2 (bases 1 to 1511)
AUTHORS He,X., Anderson,J.C., del Pozo,O., Gu,Y.-Q., Tang,X. and
Martin,G.B.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-2003) Boyce Thompson Institute, Cornell
University, Tower Road, Ithaca, NY 14853, USA
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Best Local Similarity: 91.18% Mismatches: 12
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Db 367 TCGAAGCTGATGTGAATAACTCTGTGTGATCAAGCGAGGGCTATACTTGT GG 426
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisG1 lis 60
Db 427 AATGTTCAACCGGTGAATGTCCGGTCACTGTTTGTGGTATATTCATGG AC 486
Qy 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTy et 80
Db 487 GACCTGATTGAGCTGTTTCGGATTGGAGAAATGCTCCTGATACTAATTA TG 546
Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe eu 100
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Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe le 120
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Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl rp 140
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Qy 141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleG1 le 160
Db 727 AAGTATTTTCACTGATCTTTTGGTATCTACCACTAACAGCACTGATAGA TA 786
Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHis11 eu 180
Db 787 TTCGTTTGTGATGAGGACTCTCACCCTCTCTGGATACACTGGATAAT TG 846
Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr ro 200
Db 847 GACCGTATACAAGAGGTTCCACATGAAGGGCCAATGTGTGATCTCCTGTG CA 906
Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh sp 220
Db 907 GATGATCGGTGTGGTGGGAATCTCACCTCGAGGGGCTGGTTATACCTT AT 966
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaAraG1 eu 240
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Qy 241 ValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPh ro 260
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RESULT 4
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LOCUS   AB039916
DEFINITION   Vicia faba vFPP2AC-1 mRNA for type 2A protein phosphatase-1,
complete cds.
ACCESSION   AB039916
VERSION     AB039916.1 GI:7248358
KEYWORDS    vFPP2AC-1; type 2A protein phosphatase-1.
SOURCE      Vicia faba (fava bean)
ORGANISM    Vicia faba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Vicia.
REFERENCE   1 (bases 1 to 1417)
AUTHORS     Ueno,H., Kinoshita,T., Aasanuma,M. and Shimazaki,K.
TITLE       Type 2A protein phosphatase from guard cells of Vicia faba
JOURNAL     Published Only in DataBase (2000)
REFERENCE   2 (bases 1 to 1417)
AUTHORS     Ueno,H., Kinoshita,T., Aasanuma,M. and Shimazaki,K.
TITLE       Direct Submission
JOURNAL     Submitted (08-MAR-2000) Toshinori Kinoshita, Kyushu University,
Graduate School of Sciences; Ropponmatsu 4-2-1, Fukuoka, Fukuoka
810-8560, Japan (E-mail:toshinrcb@box.nc.kyushu-u.ac.jp,
Tel:81-92-726-4763 (ex.4763), Fax:81-92-726-4644)
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Qy      21 SerGluLeuGluVallyAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluThr 40
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Qy      41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly 60
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Qy      101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySe 120
Db      556 AAAGTACGTTATAGATAGAGATTACAATTCTCAGGGGAATCATGAGAG 615
Qy      121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl 140
Db      616 ACTCAGGTGATGCTTCTACGATGAATGCTTGAGAAAGTATGGAATGC 675
Qy      141 LysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIleGly 160
Db      676 AAATTCCTTACCGACTTGTGTTGATTATTATCTCTGACCGCCCTTATTGA 735
Qy      161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisAl 180
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RESULT 5
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LOCUS     AY325817
DEFINITION   Lycopersicon esculentum protein phosphatase 2A catalytic
(P2Acl) mRNA, complete cds.
ACCESSION   AY325817
VERSION     AY325817.1 GI:34398260
KEYWORDS    Lycopersicon esculentum (Solanum lycopersicum)
SOURCE      Lycopersicon esculentum
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
ascrids; lamiales; Solanales; Solanaceae; Solanum; Lj
REFERENCE   1 (bases 1 to 1380)
AUTHORS     He,X., Anderson,J.C., Pozo Od,O., Gu,Y.Q., Tang,X. a
TITLE       Silencing of subfamily I of protein phosphatase 2A c
subunits results in activation of plant defense resp
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QY	141	LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleG	Ie 160
DB	690	AAGTAATTCACGTGCCTTTGGATTATCTACCATTGACGGCCTCATAGA	.TA 749
QY	161	PheCysLeuHisGlyClyLeuSerProSerLeuAspThrLeuAspHisII	.eu 180
DB	750	TTCGTGTTGCATGGAGGACTCTCACCATCCCTTTGATACACTTGATAACA	TG 809
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Db 1110 CAGAATTTCTTCAGTTTGACCCAGTCCACGACAGATTGAGCCTGATAC AG 1169

Qy 301 ThrProAspTyrPheLeu 306

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RESULT 6

PSY298829
LOCUS 1407 bp cDNA 1100bp
BB-2005

DEFINITION Fagus sylvatica mRNA for protein phosphatase 2A (pp2A) (pp2A).

ACCESSION	AJ298829
VERSION	AJ298829.1 GI:10638984

KEYWORDS pp2A-1 gene; protein phosphatase 2A.

SOURCE *Fagus sylvatica* (European beech)

ORGANISM *Fagus sylvatica*
Eukaryote, Vascular plant, Stranctophyta, Embryophyta, Angiosperms

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Malvales; Malvaceae; Sterculiaceae; Sterculia

rosids; eurosids I; Fagales; Fagaceae; Fagus.

REFERENCE 1

AUTHORS Gonzalez, M., Nicolas, C., Lorenzo, O., Nicolas, G. and z, D.

TITLE Characterization and expression of a protein phosphate 2A

regulated by GA3 in dormant *Fagus sylvatica* seeds
unpublished

REFERENCE 2 (bases 1 to 1497)

AUTHORS	TITLE
NICOLAS, C.	Direct Submission

JOURNAL Submitted (02-OCT-2000) Nicolas C., Fisiologia Veget de Salamaca. Plaza Doctores de la Reinas/n. 37007 Sa SPAIN ersidad

FEATURES	
Location/Qualifiers	
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ORIGIN

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US-10-764-259-13 (1-306) x FSV298829 (1-1497)

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QY 301 ThrProAspTyrPheLeu 306
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RESULT 7
AY093267
LOCUS
DEFINITION
Arabidopsis thaliana similar to protein phosphatase 1
(Atg10430) mRNA, complete cds.
ACCESSION
AY093267
VERSION
AY093267.1 GI:20259837
KEYWORDS
FLI CDNA.
ORGANISM
Arabidopsis thaliana (thale cress)
SOURCE
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eumariophyta; Magnoliophyta; eudicotyledons; core eu
rosids; eurosids II; Brassicales; Brassicaceae; Arab
1 (bases 1 to 1092)
Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., I
Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P.
Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kam
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Phai
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
Direct Submission
Submitted (26-MAR-2002) DNA Sequencing and Technolo
Stanford University, 855 California Avenue, Palo Alt
USA
e-mail for correspondence: arab@sequence.stanford.edu
RIKEN Genomic Sciences Center (GSC) members carried
collection and clustering of RAFL cDNAs (RAFL cDNA :
Arabidopsis Full-length cDNA): Seki, M., Narusaka, M
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGSC (SSP) Consortium members ca
sequencing and annotation of the RAFL cDNAs: Southwic
Nguyen, M., Karlin-Neumann, G., Lam, B., Miranda, M., P
Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chu
Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shim
Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
Southwick, A. (SSP/Stanford) and Seki, M. (RIKEN GSC)
equally to this work. Shinozaki, K. (RIKEN GSC) and
(SSP/Stanford) contributed equally to this work as
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1. .1092
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ORIGIN
Alignment Scores:
Pred. No.: 1,55e-145 Length: 1092
Score: 1522.00 Matches: 274
Percent Similarity: 95.10% Conservatives: 17
Best Local Similarity: 89.54% Mismatches: 15
Query Match: 91.14% Indels: 0
DB: 15 Gaps: 0

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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluLutrp 40
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QY 61 TCGGAGCGGATGATGAGCAGCTTTGCCATCAAGCAGAGCGATCCTTGTGAGGAAAT 120
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QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGlyGlnPheHis 60
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QY 421 AAGTATTTTACAGACCTTTTTCGATTTCTCTCTTACCGCCCTCATAGAGATCAGTT 480
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QY 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisIleArgAlaLeu 180
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QY 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTyrSerAspPro 200
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QY 541 GATCGATACAGGAGTTCCACAGGAGACCTATGTTGATTTTATTATGTTGCTGATCCT 600
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QY 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
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QY 601 GATGATCATGTGGATGGGATATCTCCACGAGGTCTGGTTATACATTTGGACAGGAT 660
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QY 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
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RESULT 8
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LOCUS Arabidopsis thaliana protein phosphatase mRNA, compl
DEFINITION M96733.1 GI:166822
ACCESSION M96733
VERSION protein phosphatase.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1264)
AUTHORS Arino,J., Perez-Callejon,E., Cunillera,N., Camps,M.,
Ferrer,A.
TITLE Protein phosphatases in higher plants: multiplicity
of phosphatases in Arabidopsis thaliana
JOURNAL Plant Mol. Biol. 21 (3), 475-485 (1993)
PUBMED 8382968
COMMENT Original source text: Arabidopsis thaliana (library:
young adult in flowering stage whole plant (includin
mRNA.

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Pred. No.: 1,87e-145 Length: 1264
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Percent Similarity: 95.10% Conservatives: 17
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Query Match: 91.14% Indels: 0
DB: 15 Gaps: 0

US-10-764-259-13 (1-306) x ATHPRPHB (1-1264)
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Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeuValAlaLeu 100

Db 438 GGAGACTATGTAGATCGTGGCTACTATTCACTAGAGACAGTTCTCTATTGTTGGCACTA 497

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Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuileGluHisGluile 160

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RESULT 10

AB039917

LOCUS

DEFINITION

Vicia faba vFP2Ac-2 mRNA for type 2A protein phosphatase-2,
complete cds.

AB039917

AB039917.1 GI:7248360

VERSION

KEYWORDS

SOURCE

ORGANISM

Vicia faba (fava bean)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Vicia.

REFERENCE

1 (bases 1 to 1475)

Ueno,H., Kinoshita,T., Asanuma,M. and Shimazaki,K.
Type 2A protein phosphatase from guard cells of Vicia faba
JOURNAL
Published Only in Database (2000)

REFERENCE

2 (bases 1 to 1475)

AUTHORS

TITLE

JOURNAL

Ueno,H., Kinoshita,T., Asanuma,M. and Shimazaki,K.
Direct Submission
Submitted (08-MAR-2000) Toshinori Kinoshita, Kyushu
Graduate School of Sciences; Ropponmatsu 4-2-1, Fuku
810-8560, Japan (E-mail:toshinob@box.nc.kyushu-u.ac
Tel:81-92-726-4763 (ex.4763), Fax:81-92-726-4644)

FEATURES

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US-10-764-259-13 (1-306) x AB039917 (1-1475)

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Db 375 AACGTGCAGCAGTGAAGTGTCCGGTCCAGGTCGCGGTGATTTACCGG

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Qy 301 ThrProAspTyrPheLeu 306

Db 1155 ACTCCAGATTATTTTGTG 1172

RESULT 11

AY087557

LOCUS AY087557 1261 bp mRNA linear PLN 14-APR-2003

DEFINITION Arabidopsis thaliana clone 36621 mRNA, complete sequence.

ACCESSION AY087557

VERSION AY087557.1 GI:21406295

KEYWORDS FLI CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 1261)

AUTHORS Haas, B.J., Volkovsky, N., Town, C.D., Troupkhan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.B.

TITLE Full-length messenger RNA sequences greatly improve genome annotation

JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)

REFERENCE 2 (bases 1 to 1261)

AUTHORS Brover, V., Troupkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

TITLE Full-length cDNA from Arabidopsis thaliana

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1261)

AUTHORS Brover, V., Troupkhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.

TITLE Direct Submission

JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A

sequence is considered to be 3'-truncated if it lacks C-terminal end of the encoded protein. Please note that sequences are derived from the Ws or Llaer ecotypes and may contain polymorphisms when compared to sequences Genset carried out the library production and sequencing full-length clones. Ceres, Inc. carried out the Clus-5' sequences, selection of clones, and sequence assembly Location/Qualifiers

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/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="36621"

153. 1073

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/db_xref="GI:21593150"

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ORIGIN

Alignment Scores:

Pred. No.: 1,22e-144 Length: 1261

Score: 1514.00 Matches: 273

Percent Similarity: 94.77% Conservative: 17

Best Local Similarity: 89.22% Mismatches: 16

Query Match: 90.66% Indels: 0

DB: 15 Gaps: 0

US-10-764-259-13 (1-306) x AY087557 (1-1261)

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Db 153 ATGCGCTCAACACGGAGATCTCGACCGTCAGATCGAACAGCTAATGGAGTG; 212

Qy 21 SerGluLeuGluValIleAsnLeuCysAspGlnAlaArgThrIleLeuVal; 40

Db 213 GGTGAAGCAGACGTAAGATCCTTTGGATCAAGCTAAGCGGATTTCTCGT; 272

Qy 41 AsnValGlnProValIleCysProValThrValCysGlyAspIleHisGly; 60

Db 273 AATGTTCAACCGGTTAAGTGTCCGTTACGGTATGCGCGGATATCCATGG; 332

Qy 61 AspLeuIleGluLeuPheArgIleGlyGlyIleValAlaProAspThrAsnTyr; 80

Db 333 GACCTAATTGAGCTATTTTCGTATTGGTGGTAAATGCTCTGTACTACTAATTA; 392

Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLeu; 100

Db 393 GGAGATTATGATCGTGGCTACTATTCTGTAGAAACAGCTCTCTCTATT; 452

Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlySer; 120

Db 453 AAGTGGCTTACAGGACAGACTTACGATCTCGGAGGGAATCATGAGAG; 512

Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgIleTyrGlyAsnAla; 140

Db 513 ACACAAGTCTATGGTTTTTATGACGAATGCTTGAGGAAATACGGAAATGCG; 572

Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleGly; 160

Db 573 AAGTATTATCGGACCTTTTCGATTATCTCTCTTAAACAGCACTCATAGA; 632

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Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGlnAsp 220
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Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGlnLeu 240
Db 813 ATTGTACTCAGTTCAATCATATCAATGAGCTGAGTCTGTATATCAAGAGCGCATCAATT 872
Qy 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPheSerAlaPro 260
Db 873 GTAATGGAAGGCTATAATTTGGTGTGAGGAAAGAACGTAGTACACAGTGTGTAGTGACCA 932
Qy 261 AsnTyrCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMetAsn 280
Db 933 AACTACTGTACAGATGTGGAACATGCGCGCAATTCTTGAGATTGGAGAAAGATGGAA 992
Qy 281 ArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArgLys 300
Db 993 CAGAACTCTCTCAATTGATTCAGACCACTAGACAAAGTCGAACCCGATACACACGCAAG 1052
Qy 301 ThrProAspTyrPheLeu 306
Db 1053 ACCCTGATTATTTTGG 1070

RESULT 12
AF107464
LOCUS
DEFINITION
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ACCESSION
AF107464
VERSION
AF107464.1 GI:3986749
KEYWORDS
Hevea brasiliensis
SOURCE
Hevea brasiliensis
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Micrandreae; Hevea.
REFERENCE
1 (bases 1 to 1370)
Shin,D.H. and Han,K.-H.
Isolation of a cDNA encoding a type 2A serine/threonine protein
phosphatase (PP2A) from Hevea brasiliensis (Accession No. AF107464)
(PK99-011)
JOURNAL
Plant Physiol. 119, 364 (1999)
REFERENCE
2 (bases 1 to 1370)
Shin,D.H. and Han,K.-H.
Direct Submission
AUTHORS
Submitted (17-NOV-1998) Kumho Life and Environmental Science
JOURNAL
Laboratory, 572 Ssangam-Dong, Kwangsan-Gu, Kwangju 506-712, Korea
FEATURES
Location/Qualifiers
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gene
CDS
ORIGIN

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Alignment Scores:

Pred. No.: 4,4e-144 Length: 1370
 Score: 1509.00 Matches: 273
 Percent Similarity: 94.12% Conservative: 15
 Best Local Similarity: 89.22% Mismatches: 18
 Query Match: 90.36% Indels: 0
 DB: 15 Gaps: 0

US-10-764-259-13 (1-306) x AF107464 (1-1370)

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Qy 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVa xp 40
Db 214 CCGAGAGCCCCAGGTCAAACTCTCTGTGATCAAGCCAGGCGATTCTCGT GG 273
Qy 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisG1 is 60
Db 274 AACGTGCAGCAGTGAATGTCCGGTCACCGTTTGGCGGTGATATTCACGG : 333
Qy 61 AspLeuIleGluLeuPheArgIleGlyLysAlaProAspThrAsnTy let 80
Db 334 GATCTCATCGAGCTCTTTAGGATAGGAGGAATGCGCCTGATACCAATTA TG 393
Qy 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe eu 100
Db 394 GCGCACTATGTAGATCGGGGTACTATTTCAGTGGAGACTGTCACTCTT TG 453
Qy 101 LysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGluSe le 120
Db 454 AAAGTTCGTACAGATAGAAATTCATATTTCTTAGGGGAATCATGAAG TC 513
Qy 121 ThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsnAl rp 140
Db 514 ACTCAAGTGTATGTTCTATGATGAGTGTCTTGAGAAATATGGAAATGC GG 573
Qy 141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleG1 le 160
Db 574 AAGTATTTCACAGATCTTTTCGATTATCTACTCTTACAGCCCTTATTGA TC 633
Qy 161 PheCysLeuHisGlyGlyLeuSerProSerLeuAspThrLeuAspHisI1 eu 180
Db 634 TTCGTTTGCAGGTGGACTTTCACCATCTTTGGATACATTAGATAATAT TG 693
Qy 181 AspArgIleGlnGluValProHisGluGlyProMetCysAspLeuLeuTr ro 200
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Qy 201 AspAspArgCysGlyTyrGlyIleSerProArgGlyAlaGlyTyrThrPh sp 220
Db 754 GATGATCGATGTGGTGGGAATATCTCTCTGTGTGTGGCTATACAT AT 813
Qy 221 IleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAl eu 240
Db 814 ATAGCTGCTCAATTCAACCATCAACATGGGCTCACTCTGATTTCCAGAGC TC 873
Qy 241 ValMetGluGlyTyrAsnTyrCysGlnAspLysAsnValValThrValPh ro 260
Db 874 GTCATGAAGGATACAACTGGTGTGAGGAAAGAAATGTGGTTACTGTATT CA 933
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Qy 301 ThrProAspTyrPheLeu 306

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Db 1054 ACCCTGATTATTTT 1071

RESULT 13
AK072676
LOCUS
DEFINITION
ORyza sativa (japonica cultivar-group) cDNA clone.J023136C13, full insert sequence.
AK072676 1563 bp mRNA linear PLN 24-JUL-2003
AK072676
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
ORyza sativa (japonica cultivar-group)
ORyza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yarak, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ohtsuka, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Atakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Sato, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)

TITLE
JOURNAL
PUBMED
12869764
REFERENCE
AUTHORS
2 (bases 1 to 1563)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Hiraoka, T., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ohtsuka, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, F., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007]
This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ohtsuka, Y., I. Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Science and Genome Science Laboratory in Riken: Adachi, J., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murakami, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Wal Yasunishi, A. and Hayashizaki, Y.
Location/Qualifiers
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ORIGIN
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Score: 1508.50 Matches: 272
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Best Local Similarity: 88.60% Mismatches: 11
Query Match: 90.33% Indels: 1
DB: 15 Gaps: 1

US-10-764-259-13 (1-306) x AK072676 (1-1563)

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QY 20 LeuSerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleIle
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QY 40 TrpAsnValGlnProValLysCysProValThrValCysGlyAspIleIle
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QY 60 HisAspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsp
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QY 80 MetGlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerIle
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QY 100 LeuLysValArgTyrArgAspArgIleThrIleLeuArgGlyAsnHisGlu
454 TTGAAGTACCTACAGAGATCGAATTAATTAATTTAGAGGAGGAATCATGA
QY 120 IleThrGlnValTyrGlyPheTyrAspGluCysLeuArgLysTyrGlyAsn
514 ATCACTCAAGTGTACGGCTTCTACGATGAATGCTTGAGAAAGTATGAAA
QY 140 TrpLysTyrPheThrAspLeuPheAspTyrIleuProLeuThrAlaLeuIle
574 TGGAAATACTTTACAGACTTGTGTTGATTATTGTCCTCTCACAGCTCTTAT
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Db      694 CTTGATCGTATACAAGAGTCTCTCATGAAGACCCATGTGTGATCTTTTGGTGGTCTGAC 753
Qy      200 ProAspAspArgCysGlyTrpGlyIleSerProArgGlyAlaGlyTyrThrPheGlyGln 219
Db      754 CCAGATGACAGATCGGGTGGGGAATTTCCACGAGAGGAGCAGGTTATACATTTGGGCAA 813
Qy      220 AspIleAlaGluGlnPheAsnHisThrAsnGlyLeuSerLeuValAlaArgAlaHisGln 239
Db      814 GATATCGCTCAACAGTTTAACCATCAAAATGGTCTCTCTCATCTCAAGGGCACATCAA 873
Qy      240 LeuValMetGluGlyTyrAsnTrpCysGlnAspLysAsnValValThrValPheSerAla 259
Db      874 CTTGTANTGAAGAGTTTAATTTGGTGTACGCAAGAATTTGTGACCGTCTTTCAGTGCA 933
Qy      260 ProAsnTrpCysTyrArgCysGlyAsnMetAlaAlaIleMetGluIleAspGluThrMet 279
Db      934 CCAAACTACTGTATCGCTGTGTAACTGGTCAATTTCTTGAGATTGGCGAAACATG 993
Qy      280 AsnArgSerPheLeuGlnPheGluProAlaProArgGlnSerGluProAspValThrArg 299
Db      994 GATCAGAACTTCTCCAAATTTGATCCAGCTCTCGGCAAAATTGAACCCAGACACACACGC 1053
Qy      300 LysThrProAspTyrPheLeu 306
Db      1054 AAGATCCCGACTACTTTTGG 1074

RESULT 14
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DEFINITION   Sequence 705 from Patent W00216655.
ACCESSION   AX506010
VERSION     AX506010.1  GI:23387247
KEYWORDS
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS     Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
TITLE       Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL     Patent: WO 0216655-A 705 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
(CH)

FEATURES
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Alignment Scores:
Pred. No.:   3,34e-144      Length:      921
Score:       1508.00      Matches:    272
Percent Similarity: 94.44%      Conservative: 17
Best Local Similarity: 88.89%      Mismatches: 17
Query Match: 90.30%      Indels:    0
DB:          6           Gaps:      0

US-10-764-259-13 (1-306) x AX506010 (1-921)

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Db      1 ATGCCGTTAAACGGAGATCTGCACCGCTCAGATCGAACAGCTAATCGAGTGTAAAGCCGTTA 60
Qy      21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuValGluGluTrp 40
Db      61 GGTGAAGCAGACGTGAAGATCCTTTGGCATCAAGCTAAAGCGATTTCTTTGTTGAGGAATAT 120

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Qy      41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGln 60
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Db      181 GACCTAATGAGCTATTTTCGTATTGGTAAATGCTCCTGATCTAAATTA 240
Qy      81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe 100
Db      241 GGAGATTATGATAGATCGTGGCTACTATTCTGTAGAAACAGTCTCTCTAT 300
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Db      301 AAGGTGCGTTACAGGACAGACTTACGATCTCGGAGGGAATCATGAGAG 360
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Db      361 ACACAAGTCTATGTTTATGCGAATGCTTGAGAAATACGGAATGTC 420
Qy      141 LysTyrPheThrAspLeuPheAspTyrLeuProLeuThrAlaLeuIleG 160
Db      421 AAGTATTTTACGGACCTTTTCGATTATCTCCTCTTACAGCAGCTCATAGA 480
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ACCESSION   AY096543
VERSION     AY096543.1  GI:20465466
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SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core e
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1 (bases 1 to 952)
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,B.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., C

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EP-2002
hatasephyta;
edons;
M.,
.,

Tang, C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R. W., Ecker, J. R., and Theologis, A.

Arabidopsis Open Reading Frame (ORF) Clones

TITLE
JOURNAL
REFERENCE
AUTHORS

2 (bases 1 to 952)
Yamada, K., Ban, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R. W., Ecker, J. R., and Theologis, A.

Direct Submission

Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan

Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

TITLE
JOURNAL
COMMENT

The Salk, Stanford, GPEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Ban, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R., and Theologis, A.

Yamada, K. (SSP/GPEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/GPEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers

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ORIGIN

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Search completed: December 9, 2005, 11:52:04

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Best Local Similarity: 88.89% Mismatches: 17
Query Match: 90.30% Indels: 0
DB: 15 Gaps: 0
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QY 21 SerGluLeuGluValLysAsnLeuCysAspGlnAlaArgThrIleLeuVal; p 40
DB 61 GGTGAACAGACGTCAGATCCTTTGGATCAAGCTAAAGCGATCTCTGT; T 120
QY 41 AsnValGlnProValLysCysProValThrValCysGlyAspIleHisGly; LS 60
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QY 61 AspLeuIleGluLeuPheArgIleGlyGlyLysAlaProAspThrAsnTy; AT 80
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QY 81 GlyAspTyrValAspArgGlyTyrTyrSerValGluThrValSerLeuLe; au 100
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QY 301 ThrProAspTyrPheLeu 306
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